

CC cell viability indicates the presence of an inhibitor and a decrease in
 CC cell viability indicates the presence of an enhancer. Optionally, the
 CC method involves detecting the presence of large and small caspase
 CC subunits after contacting cell transformed with the vector expressing
 (I), with the candidate compound. A decrease in processing indicates the
 CC presence of an inhibitor and an increase in the processing indicates the
 CC presence of an enhancer. Preferably, the large and small subunits of
 caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for
 CC identifying a compound that inhibits Smac binding to Smac-binding
 molecule (a portion of IAP e.g. a BIR domain such as BIR1, BIR2 or BIR3,
 CC or a full-length IAP). (II) is useful in gene therapy techniques. The
 CC present sequence represents the amino acid sequence of Smac protein.
 XX

SQ Sequence 239 AA;

Alignment Scores:

Pred. No.: 3.17e-105

Length: 239

Score: 1201.00

Matches: 239

Percent Similarity: 100.00%

Conservative: 0

Best Local Similarity: 100.00%

Mis matches: 0

Query Match: 49.10%

Indels: 0

DB: 23

Gaps: 0

US-09-939-293-1 (1-1358) x AAU78447 (1-239)

QY 20 ANGGGGCTCTGAACAGTTCGCTGCGCAGCGTAACTTCTCAGGTACAGACAG 79

Db 1 MetalAlaLaleuLysSerTripleLeuSerArgSerValnSerPhePheArgTyArgIn 20

QY 80 TGTGTTGTTGTTCTCCGTTGCGCTACTTTAAGAGGCGCTTTCAGATAAGA 139

Db 21 CysLeuCysValProValAlaAsnPhelLysSargCysPheSerGluLeuLeuArg 40

QY 140 CATGCCACAAACTGTGAGGATGCGCTTGAGATAACCTGTGCGGTCTATGCA 199

Db 41 ProThPheSthValThrLysPheGlyAlaThrLysCysAlaValProLea 50

QY 200 CAGAACATCAGAACCTCATTCCTTAGTAGTGAACTGATGAGAGGAGGAGGAGTGTG 259

Db 61 GluLysSerGluProHisSerLeuSerGluAlaLeuMetArgGalaValSerLeu 80

QY 260 GTGACAGATAGCACCTCTACTTCTCTCTCTGAGCACATATCACAGTTA 319

Db 81 ValThrAspSerThrSerThrPheLeuSerGlnThrThrTyRAlaLeuLeuLysGluAla 100

QY 320 ACTGATATCTAAAGCTGTATRACTCTRACTCTCTAACCGACAATATCACAGTTA 379

Db 101 ThrglyTyThrLysAlaValTyRlethrSerLeuLeuArgGlnTyThrSerLeu 120

Db 380 CTGGGAAATTGAATTCAAGAGGAGATGAGGTGGCAAGGTGATCATAGGCCAGA 439

Db 121 LeuGlyLysMetAsnSerGluLysGluLysAspGluValTrpGlnValleIleGlyAlaArg 140

QY 440 GCTGAGATEGACTCAAACACCAGAGTACTGAGCTGAGTGAACCACTTGAGTC 499

Db 141 AlaGluMetThrSerLysHisGlnIutYrLeuLysLeuGluThrThrPheThrAla 160

QY 500 GTGCTCTTCAGAGTGGCAGACGTCATCAACTGGCCAGATCAGGCC 559

Db 161 ValGlyLeuSerGluMetAlaAlaGluAlaAlaTyRlethrGlyAlaLysGlu 180

QY 560 ATAACGCCAGGAATCACATTCACTGGAACTGAGCTGGCAGCTGCACAGTC 619

Db 181 IleThrAlaArgAsnHisIleGlnLeuValLysLeuGlnValGluValHisGlnLeu 200

QY 620 TCCCGGAAGCCAGAACCAAGCTGCAGAGCACAGATGAGAGCTCGTCAGAAC 679

Db 201 SerArgLysAlaGluThrLysLeuAlaLysAlaGlnIutLysLeuArgGlnLysThr 220

QY 680 CAGGAGGAAGGGAGGAGCCGCTGAGTCGGAGGAGCCACTGCGTGGAGAT 736

Db 221 GluGluGluLysGluLysGluGlnGluLysGluLysGluLysGluLysGlu 239

RESULT 3

NAB54139

ID AAB54139 standard; Protein; 227 AA.

XX

AC AAB54139;

XX DT 09-MAR-2001 (first entry)

XX DE Human pancreatic cancer antigen protein sequence SEQ ID NO:591.

XX KW Human; Pancreas; Pancreatic cancer; Pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.

XX OS Homo sapiens.

XX PN WC200055320-A1.

XX PD 21-SEP-2000.

XX PF 08-MAR-2000; 2000WO-US05989.

XX PR 12-MAR-1999; 99US-0124270.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI; 2000-57944/54.

DR N-PSDB; AAC98904.

XX PT New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition -

XX PS Claim 11; Page 1027-1028; 137pp; English.

XX CC AAC9873 to AAC9231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nontropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be screened for. The pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC9873 to AAC9240 and AAB5467 represent sequences used in the exemplification of the present invention.

XX SQ Sequence 227 AA;

Alignment Scores:

Pred. No.: 2.98e-99

Length: 227

Score: 1138.00

Matches: 226

Conservative: 0

Mis matches: 0

Best Local Similarity: 100.00%

Query Match: 46.52%

Indels: 0

DB: 21

Gaps: 0

CC candidate enhancer; and detecting cell viability, where an increase in cell viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an enhancer. Optionally, the method involves detecting the presence of large and small caspase subunits after contacting cell transformed with the vector expressing (I), with the candidate compound. A decrease in processing indicates the presence of an inhibitor and an increase in the processing indicates the presence of an enhancer. Preferably, the large and small subunits of caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for identifying a compound that inhibits Smac binding to Smac-binding molecule (a portion of IAP e.g., a BIR domain such as BIR1, BIR2 or BIR3, or a full-length IAP). (II) is useful in gene therapy techniques. The present sequence represents the N-terminal amino acid sequence of Smac protein.

XX

CC	Sequence	40 AA;
CC	SQ	
CC	Alignment Scores:	
CC	Pred. No.:	1.56e-09
CC	Score:	190.00
CC	Percent Similarity:	100.00%
CC	Best Local Similarity:	100.00%
CC	Query Match:	7.77%
CC	DB:	23
CC	US-09-939-293-1 (1-1358) x AAU78430 (1-40)	
CC	QY 185 GCGGGTTCTCATATGACAGAAATCAGAGCTCTATTCCCTTAGTAGTGAAGCATGTGGG 244	
CC	Db 1 AlavalProteAlaGlnlySSerGluProHisSerleuseSerSerGluAlaLeuMetArg 20	
CC	QY 245 AGAGCGAGTGCTTGGTACAGATGCCCTACTCTCTCTAGACCACATAGCG 304	
CC	Db 21 ArgAlavalSerLeuValThrAspSerThrSerThrPheLeuSerGlnThrThrTyrAla 40	
XX	RESULT 6	
XX	AAU78436	
XX	ID AAU78436 standard; Peptide: 39 AA.	
XX	XX	
XX	AC AAU78436;	
XX	XX	
XX	DT 18-JUN-2002 (first entry)	
XX	DE Inhibitor of apoptosis (IAP) protein Smac, mutant Smac-N39.	
XX	KW Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2; Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy; neoplastic cell; mutant; tumour.	
XX	OS Homo sapiens.	
XX	OS Synthetic.	
XX	PN WO200216418-A2.	
XX	PD 28-FEB-2002.	
XX	PF 24-AUG-2001; 2001WO-US26492.	
XX	PR 24-AUG-2000; 2000US-227735P.	
XX	PA (UYKE-) UNIV JEFFERSON THOMAS.	
XX	PI Alnemri ES;	
XX	DR WPI; 2002-304115/34.	
PT Novel Smac peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which over-expresses inhibitor of caspase, and for identifying apoptosis modulating compounds -		
PT Example 3: Fig 7; 70pp; English.		

CC The invention relates to an isolated Smac peptide or polypeptide (I) and an isolated nucleic acid (II) encoding (I). Also described is a method of identifying a compound that inhibits apoptosis, comprising:

CC (a) separately contacting several cell populations expressing a cytosolic Smac (a Smac isoform that begins with MKSDIF sequence, replacing the mitochondrial targeting sequence (residues 1-55 of (I)), and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting domain) with a compound to be tested for apoptotic inhibiting activity;

CC (b) incubating the cell populations with a direct stimulus of the cell death pathway; and (c) measuring the specific apoptotic activity of the cell populations, where inhibition of the specific apoptotic activity is indicative that the compound is an inhibitor of apoptosis. (I) and (II) are useful for inducing apoptosis in a cell. The Smac polypeptide and polynucleotide are useful for stimulating apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase, where the inhibitor inhibits activation or activity of caspase-3, caspase-7 or caspase-9. Preferably, the cell overexpresses at least a portion of IAP.

CC (I) is useful for identifying an inhibitor or enhancer of a caspase-mediated apoptosis which involves contracting a cell transformed or transfected with a vector expressing (I) with a candidate inhibitor or candidate enhancer; and detecting cell viability, where an increase in cell viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an enhancer. Optionally, the method involves detecting the presence of large and small caspase subunits after contracting cell transformed with the vector expressing (I), with the candidate compound. A decrease in processing indicates the presence of an inhibitor and an increase in the processing indicates the presence of an enhancer. Preferably, the large and small subunits of caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for identifying a compound that inhibits Smac binding to Smac-binding molecule (a portion of IAP e.g. a BIR domain such as BIR1, BIR2 or BIR3, or a full-length IAP). (II) is useful in gene therapy techniques. The present sequence represents the amino acid sequence of Smac mutant Smac-N39.

XX - Sequence 39 AA;

SQ Alignment Scores:

Pred. No.:	3.71e-09	Length:	39
Score:	186.00	Matches:	39
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	7.60*	Indels:	0
DB:	23	Gaps:	0

US-09-939-293-1 (1-1358) x AAU78436 (1-39)

QY 185 GCGGTCTTATTGACAGAAATCAGAGCTCAATTCCTTAGTACTGAACCATGATGAGG 214

Db 1 AlavalProleAlaglnlyssergluProhisSerLeuserGluLaleMetarg 20

QY 245 AGACAGCTGTTGGTACAGATGACCTCTACTCTCTCTGACACCATAT 301

Db 21 ArgAlavalSerLeuValThrAspSerthrSerThrPheLeuserGlnLthrrnTyr 39

RESULT 7

RAU78439

ID AAU78439 standard; Peptide: 35 AA.

XX AAU78439;

XX 18-JUN-2002 (first entry)

DE Inhibitor of apoptosis (IAP) protein Smac, peptide Smac-N35.

XX Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2; Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy; neoplastic cell; tumour.

XX Homo sapiens.

XX WO20021618-A2.

XX

PD 28-FEB-2002.

XX

PF 24-AUG-2001; 2001WO-US26492.

XX

PR 24 AUG-2000; 2000US-22735P.

XX PA (UYE-) UNIV JEFFERSON THOMAS.

XX PI Almamri ES;

XX DR WPI; 2002-304115/34.

PS Example 4; Page 47; 78pp; English.

XX The invention relates to an isolated Smac peptide or polypeptide (I) and an isolated nucleic acid (II) encoding (I). Also described is a method of identifying a compound that inhibits apoptosis, comprising:

CC (a) separately contacting several cell populations expressing a cytosolic Smac (a Smac isoform that begins with MKSDIF sequence, replacing the mitochondrial targeting sequence (residues 1-55 of (I)), and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting domain) with a compound to be tested for apoptotic inhibiting activity;

CC (b) incubating the cell populations with a direct stimulus of the cell death pathway; and (c) measuring the specific apoptotic activity of the cell populations, where inhibition of the specific apoptotic activity is indicative that the compound is an inhibitor of apoptosis. (I) and (II) are useful for inducing apoptosis in a cell. The Smac polypeptide and polynucleotide are useful for stimulating apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase, where the inhibitor inhibits activation or activity of caspase-3, caspase-7 or caspase-9. Preferably, the cell overexpresses at least a portion of IAP.

CC (I) is useful for identifying an inhibitor or enhancer of a caspase-mediated apoptosis which involves contracting a cell transformed or transfected with a vector expressing (I) with a candidate inhibitor or candidate enhancer; and detecting cell viability, where an increase in cell viability indicates the presence of an inhibitor and a decrease in cell viability indicates the presence of an enhancer. Optionally, the method involves detecting the presence of large and small caspase subunits after contracting cell transformed with the vector expressing (I), with the candidate compound. A decrease in processing indicates the presence of an inhibitor and an increase in the processing indicates the presence of an enhancer. Preferably, the large and small subunits of caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for identifying a compound that inhibits Smac binding to Smac-binding molecule (a portion of IAP e.g. a BIR domain such as BIR1, BIR2 or BIR3, or a full-length IAP). (II) is useful in gene therapy techniques. The present sequence represents the amino acid sequence of Smac peptide Smac-N35.

XX - Sequence 35 AA;

SQ Alignment Scores:

Pred. No.:	4.36e-07	Length:	35
Score:	164.00	Matches:	35
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	6.70*	Indels:	0
DB:	23	Gaps:	0

US-09-939-293-1 (1-1358) x AAU78439 (1-35)

QY 185 GCGGTCTTATTGACAGAAATCAGAGCTCAATTCCTTAGTACTGAACCATGAGG 244

Db 1 AlavalProleAlaglnlyssergluProhisSerLeuserGluLaleMetarg 20

QY 245 AGACAGCTGTTGGTACAGATGACCTCTACTCTCTGACACCATAT 289

Db 21 ArgAlavalSerLeuValThrAspSerthrSerThrPheLeuserGlnLthrrnTyr 35

Alignment Scores:		Length:	
Pred. No.:	0.00562	Matches:	502
Score:	125.50	Conservative:	74
Percent Similarity:	35.00%	Mismatches:	24
Best Local Similarity:	26.43%	Indels:	102
Query Match:	5.20%	Gaps:	80
DB:	22		
US-09-939-293-1 (1-1358) x AAM52315 (1-502)		Length:	502
QY	1291 CCTTCCTCTTACTAGTAGATAAGGTT--TTACACTCCTGGCTCACGCTCACAGAC 1235	Matches:	74
Db	205 ProAspIleThrSerSerArgTyRArgGlyLeuProAlaProGlyProSerProAlaAsp 224	Conservative:	111
QY	1234 -----AGTGGGGCAGATCAGAGAACACATAGAAATCATACAAAGAACCTGTC 1184	Mismatches:	24
Db	225 LysLysArgSerGlyLysLysLysLysIleSerLysAlaAspIleGlyAlaProSerGlyPhe 244	Indels:	102
QY	1183 AACCTGGACAGGTCCCTCCCCCTGCCAC-----AAGTGCACTCCACAGA 1136	Gaps:	13
Db	245 Lys-----HisValSerHisValGlyLysPaspProGlnAsn 256		
QY	1135 GGGACAAGTACTAAATCATTTTGACGACGPAAPAGCTGAAACAGGTAAACAGT 1076		
Db	257 Gly-----pheAspValAsnAsnLeuAspProAspLeuArgSer 269		
QY	1075 TGTGACTTAAAGGCTGACAAAAGGCTCTCTCTGACCCAGTAGGCCAAATGC 1016		
Db	270 LeuPheSerArgAlaGlyIleSerGlu-----AlaGinLeu 281		
QY	1015 TTTGGGGTGGTAAAAAAATGGTAAGAACAGCACGCGTACAGAGTGGT----- 965		
Db	282 ThrAspAlaGluThrSerLysIleUtyraspHeIleGluAspGlyGlyLeuGlu 301		
QY	964 -----GAATGTAAACAGGGTGGAGTGC 935		
Db	302 AlaValArgInglumetArgArgGlnIleProLeuProProProProSerArg 321		
QY	934 GCTAAGACAGCTCCAGGGCAGGCCCTGAGACACAGAGGACTCACAGCTCACAAAG 875		
Db	322 GlyGlyAsnGlnLeuProArg--ProProIleValGlyGlyAsnlys----- 336		
QY	874 CGTCTCGCTGATGGCCAGGCGAGCT-----GCGCC 839		
Db	337 -----GlyArgSerGlyProLeuProProValProLeuGlyIleAlaPro 351		
QY	838 TCTTCCTGGTGCAACAGACATGCCAACCTGGCAGGGGCATCTGCCCTGCTT 779		
Db	352 ProProProIleProArgGlyProProProProGlyArgGlyIleProProPro 371		
QY	778 CCCCACTGAGGGAGACAGGGCAGTGTCTCAGGCCCTCATCTCACGAGGAGG 719		
Db	372 ProProAlaLysGlyArgSerGlyProLeuProProPro-ProGlyAlaGlyIle 391		
QY	718 CTCCCTCTGCACTCAGGCCCTCCCTCCCTCTGTTCTGACGGAGCTCTTC 659		
Db	391 IleProMetProProProProProProProProProProProPro 407		
QY	658 TATCCTGCTCTGCCAGCTGGTTCTGCCCTTCAGGCCCTCATCTCACGAGGAC 599		
Db	408 -----AsnGlyProAlaProProProProLeuPro 417		
Alignment Scores:		Length:	502
Pred. No.:	0.00562	Matches:	74
Score:	125.50	Conservative:	111
Percent Similarity:	35.00%	Mismatches:	24
Best Local Similarity:	26.43%	Indels:	102
Query Match:	5.20%	Gaps:	80
DB:	22		
US-09-939-293-1 (1-1358) x AAG67333 (1-502)		Length:	502
QY	1291 CCTTCCTCTTACTAGTAGATAAGGTT--TTACACTCCTGGCTCACGCTCACAGAC 1235	Matches:	74
Db	205 ProAspIleThrSerSerArgTyRArgGlyLeuProAlaProGlyProSerProAlaAsp 224	Conservative:	111
QY	1234 -----AGTGGGGCAGATCAGAGAACACATAGAAATCATACAAAGAACCTGTC 1184	Mismatches:	24
Db	225 LysLysArgSerGlyLysLysLysIleSerLysAlaAspIleGlyAlaProSerGlyPhe 244	Indels:	102
QY	1183 AACCTGGACAGGTCCCTCCCCCTGCCAC-----AAGTGCACTCCACAGA 1136	Gaps:	13
Db	245 Lys-----HisValSerHisValGlyLysPaspProGlnAsn 256		
QY	1135 GGGACAAGTACTAAATCATTTTGACGACGTAATAAGCTGAAACAGGTAAAC 1076		
Db	257 Gly-----pheAspValAsnAsnLeuAspProAspLeuArgSer 269		

Best Local Similarity:	26.79%	Mismatches:	125
Query Match:	4.64%	Indels:	101
DB:	21	Gaps:	17
US-09-939-293-1 (1-1358) x AAY69166 (1-1485)			
QY 537 TGATGCGACCTCTGCTGAGAACACTGCAAGTGGTTTC 478			
Db 240 -----ValThrSerSerTrpProPr 246			
QY 477 AGCTTCAGTACT 465			
Db 246 oThrArgArgThr 250			
RESULT 15			
AAV69166 standard; Protein; 1485 AA.			
XX			
QY AAY69166;			
XX			
DT 30-MAY-2000 (first entry)			
DE A mature human N-acetylglucosaminyl transferase protein.			
XX			
KW Human; N-acetylglucosaminyl transferase V; GlcNAc-TV-b; GlcNAc-TV-c; oligosaccharide; cancer; solid tumour; tumour metastasis; infection; haematopoietic progenitor cell growth; chemotherapy; radiation therapy; proliferative disorder; neurological disorder; Kaposi's Sarcoma.			
XX			
OS Homo sapiens.			
XX			
PN WO200008171-A1.			
XX			
PD 17-FEB-2000.			
XX			
PF 05-AUG-1999; 99WO-CA00711.			
XX			
PR 07-AUG-1998; 98US-0095919.			
XX			
PA (GLYC-) GLYCODESIGN INC.			
XX			
PD 955 AACAGGGTGC-----AGTGCCCAAGGGCTAAGRACCAAGCAGTCCAGCGCAGGCTGAG 905.			
XX			
PF 115 ---GLYCYSRpsrGlySerThrProhrSerSerThrArgThrSerAlaGluLeuI 133			
XX			
PR 904 ACCACAGGAGGCACTCACAGCTCACAAAGGGCTCGCC----- 865.			
XX			
PA 133 nThrRhrAlaLeuProGluAlaHisAlaProGlnSerProPheAlaProAsnAl 153.			
XX			
QY 864 -----GATGG-----CCAGGGCAGGACCTGCCGCTCT 836			
XX			
Db 153 aThrRhsLeuGluTrpAlaArgAsnThrSerLeuAlaProGlyAla---TrProProAl 172			
XX			
QY 835 TCTCGTGTGACAGAAAGTCAGGCCAACCCCTGGCAAGGTGGCATCTGCCCTGGCTTCCC 776			
Db 172 gThrProCysGlyProGlyTrpProCysLeuGlyGlyProAlaProThrProAla--- 190			
XX			
PS Novel isolated N-acetylglucosaminyl transferase nucleic acid sequences useful for monitoring cancer and treating proliferative disorders -			
XX			
PT Claim 8; Page 50-60; 82pp; English.			
XX			
CC The present sequence represents a human N-acetylglucosaminyl transferase			
CC v protein, designated GlcNAc-TV-b. The specification also describes			
CC GlcNAc-TV-c. The proteins of GlcNAc-TV-b or GlcNAc-TV-c proteins can be			
CC used for preparing oligosaccharides. The polynucleotide and polypeptide			
CC sequences can also be used in compositions for treating a condition			
CC mediated by a GlcNAc-TV-b or GlcNAc-TV-c protein. They can be used to			
CC monitor conditions such as cancer (e.g. solid tumours, such as breast and			
CC uterine cancer) by detecting and localizing the nucleic acids. They may			
CC be used to treat or prevent cancer, inhibit or treat tumour metastasis,			
CC stimulate haematopoietic progenitor cell growth, confer protection			
CC against chemotherapy and radiation therapy in a subject, and/or treat			
CC proliferative disorders, microbial or parasitic infections, or			
CC neurological disorders. They may be particularly useful for treating			
CC cervico-uterine cancer, cancer of the kidney, brain, stomach, lung,			
CC rectum, breast, bowel, gastric, liver, thyroid, neck, cervix, salivary			
CC gland, bile duct, pelvis, mediastinum, urethra, bronchogenic, bladder,			
CC oesophagus, and colon, and Kaposi's Sarcoma which is a form of cancer			
XX associated with HIV-infected patients with AIDS.			
SQ Sequence 1485 AA;			
Alignment Scores:			
Pred. No.: 0.165	Length: 1485		
Score: 112.00	Matches: 90		
Percent Similarity: 32.74%	Conservative: 20		

Thu Feb 20 16:18:47 2003

us-09-939-293-1.rag

Search completed: February 20, 2003, 14:57:10
Job time : 81.5 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 20, 2003, 14:53:58 ; Search time 45 Seconds
(without alignments)
5802.246 Million cell updates/sec

Title: US-09-939-293-1

Perfect score: 2446

Sequence: 1 ggcttcggcgctgcacaa.....ggacttaacacagaaaaaa 1358

Scoring table: BLOSUM62

Xgapop	Xgapext	Ygapext	Fgapop	Fgapext	Delop
10.0	0.5	0.5	6.0	7.0	6.0
					Delext

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgp2_1/xuspro/spool/US099393/runat_20022003_111511-14892/app-query.fasta_1.1543
-DB=PIR_73 -SUFFIX=fastan
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40_cdi -LIST=45
-DOCALLG=200 -THR_SCORE_PCT=-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0993923_@CGN_1-175_@unl_20022003_111511-14892 -NCPU=6 -ICPU=3
-NODLXPKY -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THRESHOLD=10 -XGAPEXT=0.5 -FGRPOP=6 -FGRPEXT=7
-YGAPP=10 -YGAREXT=0.5 -DELOP=6 -DELEXT=7
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Database :

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PIR_73:*
1: pir1:*
2: pir2:*
3: Pir3:*
4: pir4:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	125.5	5.2	502 2	Wiskott-Aldrich syndrome protein WASP - human
C 2	123	5.1	805 2	hypothetical protein
C 3	116.5	4.8	1133 2	hypothetical protein
C 4	112	4.6	3660 1	dystrophin, muscle
C 5	111	4.6	1323 2	N-methyl-D-aspartate
C 6	111	4.6	1356 1	N-methyl-D-aspartate
C 7	107.5	4.4	1396 2	hypothetical protein
C 8	106.5	4.4	1520 2	hypothetical protein
C 9	105.5	4.3	3164 1	UL36 protein - hum
C 10	105	4.3	4574 2	plectin - human
C 11	105	4.4	337 2	ESPR-like protein
C 12	105	4.3	791 2	hypothetical protein
C 13	104.5	4.3	517 2	3C18c protein - conserved hypothet
C 14	104.5	4.3	581 2	E75383

RESULT 1

A55197

Wiskott-Aldrich syndrome protein WASP - human

C;Species: Homo sapiens (man)

C;Accession: A54747; A55197; I38931

R;Derby, J.M.J.; Ochs, H.D.; Francke, U.
cell 78, 635-644, 1994

A;Title: Isolation of a novel gene mutated in Wiskott-Aldrich syndrome.

A;Reference number: A54747; MUID:94349367; PMID:809912

A;Accession: A54747

A;Molecule type: mRNA

A;Cross references: GB:U12707

A;Note: this sequence is corrected in reference A55197
R;Derby, J.M.J.; Ochs, H.D.; Francke, U.
Cell 79, 922a, 1994

A;Reference number: A55197

A;Contents: erratum

A;Accession: A55197

A;Molecule type: mRNA

A;Residues: 'A' 330-366, 'LHHHPLQLQDVIDKPHPLEVGHPCRH', 'HRHRRRRPAPGMQDPLHSLL'

A;Cross-references: GB:U12707; NID:6695150

A;Note: the translated sequence in GenBank entry HSU12707 (PIDN:AAA62663.1) differs from R;Kwan, S.P.; Hagemann, T.L.; Radtke, B.E.; Blaese, R.M.; Rosen, F.S. Proc. Natl. Acad. Sci. U.S.A., 92, 406-4110, 1995

A;Title: Identification of mutations in the Wiskott-Aldrich syndrome gene and characterization of the gene product. R;Derby, J.M.J.; Ochs, H.D.; Francke, U.; Kwan, S.P.; Hagemann, T.L.; Radtke, B.E.; Blaese, R.M.; Rosen, F.S. Proc. Natl. Acad. Sci. U.S.A., 92, 406-4110, 1995

A;Reference number: I38931; MUID:95273432; PMID:7753869

A;Accession: I38931

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 'A' 1-502 <KWA>

A;Cross-references: ENBL:U19927; NID:9854672; PIDN:AAAC50140.1; PMID:9854673

C;Genetics: A;Gene: GDB:WAS; IMD2; WASP

A;Cross-references: GDB:120736; OMIM:301000

A;Map position: Xp11.23-Xp11.22

A;Note: defects in this gene may result in Wiskott-Aldrich syndrome

jagged protein prehypothetical proteo plectin [imported] hypothetical prote lamin B2 - mouse probable primosoma ankyrin 2, neurona zonadhesin - mouse keratin type II m myosin heavy chain hypothetical prote hypothetical prote hypothetical prote myosin heavy chain cellulos synthase LRG5 protein - Chl choline binding pr ankyrin 3, long sp myosin heavy chain chloride channel P limb deformity (ld DNA-binding regula chitinase (EC 3.2.1.2) hypothetical prote probable membrane neurofilament trip neurofilament trip neurofilament trip polyketide synthas hypothetical prote protein T04A8.13.1

C;Keywords: immunodeficiency

Alignment Scores:

Pred. No.: 0.0328

Length: 502

Matches: 74

Percent Conservative: 24

Score: 35.008

Best Local Similarity: 26.438

Query Match: 5.208

US-09-939-293-1 (1-1358) x A55197 (1-502)

Qy 1291 CCTTCCTCTTACTAGTATAGTT--TTCACTCCCTGGCCTCAGCTGTOCTCACAGGAC 1235

Db 205 ProAspIleValProSerArgTyrrargIleLeuProAlaProGlyProSerProAlaAsp 224

Qy 1234 -----AGTGGGGCAGATCAGAGAACACCATGAGATACTACATACAAAGAATGTC 1184

Db 225 LysLysArgSerGlyLysLysLysLysSerLysAlaAspIleGlyAlaProSerGlyPhe 244

Qy 1183 AACUCCGGACAGGTTCCTCCCTCCCGGCCAC-----AGTGGCATCCACAGA 1136

Db 245 Lys-----HisValserHisValGlyItpaspProGlnAsn 256

Qy 1135 GGAACAAGTACTAAATCATTTTGACGAGCTAAATAAGCTGAAACAGGTAAACAGT 1076

Db 257 Gly-----PheAspIvalAsnAsnIleuAspProAspIleArgSer 269

Qy 1075 TGCIGAACTTAAGGCATGACAAAGACTCTCTCTGAGCCAGGTAGGCAAATGC 1016

Db 270 LeuPheSerArgAlaGlyIleSerGlu-----AlaGlnLeu 281

Qy 1015 TTGGGTGTAGGTAAAAAAATGGTAGACAGCACGCTGAGCTGGGT----- 965

Db 282 ThraSpaIalGluThrSerIleUrleItyrasPheIleGluAspGlnGlyIleGlu 301

Qy 964 -----GAAATGTTAACAGGGTGCAGGCCA-----AGG 935

Db 302 AlaValArgGlnGluMetAlaGargIleGluIleProIleProProProProSerArg 321

Qy 934 GCTAAGAACCGAGTCCAGGCCAACGCTGAGACACAGGAGGCACTCACAGCTACAAGG 875

Db 322 GlyGlyAsnGlnIleProArg---ProProIleValGlyIleAsnLys----- 336

Qy 874 CGTCTCGCCCTGATGCCAGGGCAGGACCT-----GCCGCC 839

Db 337 -----GlyArgSerGlyProIleProProValProLeuGlyIleLeuIlePro 351

Qy 838 TCTTCAGGGGACACAGACTCATGCCAACCTGGCAGGGTGCATCNCCTCGCTT 779

Db 352 ProProProThrProArgGlyIleProProProProProProPro 371

Qy 778 CCCCACTGAGCTGGAGACAGGGCAGTCTGCTAGGCCCTCAATCTCACGCAGTAGGC 719

Db 372 ProProAlaThrGlyArgSerGlyProIleProProPro---ProGlyIleGlyIle 391

Qy 718 CTCCCTCTCCGAGTCAGCCGCTCTCCCTCTGTTCTGAGGGACTCT 659

Db 391 roProMetProProProProProProProProProProProProPro 407

Qy 658 TATCCTGCTCTGCCAGCTGCTGCTGCTGCCGAGCNGTGCACCTCCAC 599

Db 408 -----AsnGlyProIleProProProLeuPro 417

Qy 598 CTGAGTTTCACCAAGCTGAATTGATTCCTGCGGTTATAAGGCCATGATC 548

Db 417 roIleLeuValProAla-GlyGlyIleLeuAlaProGlyIleGlyIleAla 434

C;Accession: T49385

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu

submitted to the Protein Sequence Database, May 2000

A;Reference number: Z25022

A;Accession: T49385

A;Status: preliminary

A;Molecule type: DNA

A;Cross-references: EMBL:AL355927; GSPPB:GN00116; NCSP:B1D1.390

A;Experimental source: BAC clone B1D1; strain OR74A

C;Genetics:

A;Gene: NCSP:B1D1.390

A;Map position: 6

A;Introns: 54/3; 212/3

Alignment Scores:

Pred. No.: 0.0554

Length: 805

Matches: 49

Percent Conservative: 18

Score: 42.418

Best Local Similarity: 31.018

Query Match: 5.108

DB: 19

Gaps: 6

US-09-939-293-1 (1-1358) x T49385 (1-805)

Qy 927 ACCAGGTCCAGCGCAGCCCTGAGCACAGGACTACAGCTCACAAGGGCTCG 868

Db 403 ThraArgLysSerAlaThrProThrProSerGlnThrGlyIleProGlnProProIleAla 422

Qy 867 CCTGATGTCGCGCAGGCAGGACTCTCGCCGCTCTCTGGGCAACAGACTCATGCCAAC 808

Db 423 ThrProIleProProProAlaValProProValAlaGlyIleAlaProThrProProIleAla 442

Qy 807 CTGGCAGGAGTCATCCGCCGCTCTGGGCA-----CTGAGTGGGA 763

Db 443 Ala-AlaAlaGlySerIleLeuAlaAlaLeuProProValAlaAlaValLeuIleArgSerGln 462

Qy 762 GACA-----GGCACTGTCGCT-----CAGGCCCTCAATCTCACGCCAGG 724

Db 462 nThrProThrValGlyProAlaAlaProProProLeuGluAlaProLySProAlaAlaLase 482

Qy 723 TAGGCTCCCTGCTCGACTGAGCCGCTCTCCCTCTCCCTCTGTTCTGAGGGAGCCTGTTCTGAGGGAC 664

Db 482 rAlaProProThrValProAlaAlaAlaPro---AlaProValSerAsnProSerAl 501

Qy 663 TCTCTCTATCGTGTCTCCAGGTTCTGTTCTGGGAGAGCTGTTGTCGACCTCT 604

Db 501 aLeuIleAlaMetIleIleArgGlnSerGlyIleLeuSerGlyIleThrProAlaAlaProAl 521

Qy 603 TCCACCTGCACTTCACCAAGCTGAATGCTGATGCT-----TCTCTGGGGTTATAGAGGCCCTGA 550

Db 521 aProValAlaIleAlaProAlaAlaAlaProAlaAlaAlaAlaProThrHyr-----Th 538

Qy 549 TCTGGCCACTTGTATGAGCTCTGTCGCTCTCTGGAAGACCACTG 498

Db 538 rLeuIysGlnPheArgGlyIleProGlnIleLeuIleAsnArgLeuIleAspIle 555

RESULT 3

hypothetical protein F59a2.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C;Accession: T22976; 123157

R;Lightning, J.

submitted to the EMBL Data Library, June 1994

A;Reference number: Z19645

A;Accession: T22976

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1133 <WIL>

A;Cross-references: EMBL:Z34801; PIDN:CAA84332.1; GSPPB:GN0021; CESP:F59a2.6

A;Experimental source: clone F59a2

R;Burton, J.

RESULT 2

T49385

hypothetical protein Bib1.390 [imported] - Neurospora crassa

C;Species: Neurospora crassa

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

hypothetical protein K12D12.1 - caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
 C;Accession: T23620; T28109
 R;Coles, L.
 submitted to the EMBL Data Library, April 1995
 A;Accession: T23620
 A;Status: preliminary; translated from GB/EMBL/DBBJ
 A;Molecule type: DNA
 A;Residues: 1-1520 <WIL>
 A;Cross-references: EMBL:Z49069; PIDN:CAA88867.1; GSPDB:GN00020; CESP:K12D12.1
 A;Experimental source: clone K12D12
 R;Swinburne, J.
 A;Residues: 1-1520 <W12>
 A;Cross-references: EMBL:Z70213; PIDN:CAA94177.1; GSPDB:GN00020; CESP:K12D12.1
 A;Experimental source: clone ZK930
 A;Gene: CESP:K12D12.1
 A;Map position: 2
 A;Introns: 34/1; 146/2; 390/3; 471/3; 611/2; 1351/3; 1486/2
 C;Superfamily: eukaryotic type II DNA topoisomerase (ATP-hyd)
 Alignment Scores:
 Pred. No.: 1.12 Length: 1520
 Score: 107.50 Matches: 70
 Percent Similarity: 37.42% Conservatives: 49
 Best Local Similarity: 22.01% Mismatches: 110
 Query Match: 4.39% Indels: 89
 DB: 2 Gaps: 15
 US-09-939-293-1 (1-1358) x T23620 (1-1520)
 Qy 92 CCCTGTTGCGCTAATTTAGAAGCAGGGCTTCAGAGTGTAAAGACATGGCACAA 151
 Db 987 Provallevalasptvlysglu-----Typhisthr 997
 Qy 152 ACTGTGAGGATGGCTTGAGAACCTGTGCGGTTCTATGCAAGAACAGAG 211
 Db 998 AspThrThrValLysPheValValLysIleSerProGlyLysLeuargGluleuGluArg 1017
 Qy 212 CCTCATGCCCTGTAGT-----GAAGCATGTGAGGAGACAGTGCTCTTG 259
 Db 1018 GlyGlnAspLeuIleGlnValPhylsLeuGlnAlaValIleAsnThrThrCysMetVal 1037
 Qy 260 GRACAGATAGCACCTCTTACCTTCTCTCAGACCACATGGCTGATTGAACCTT 319
 :::: ||::: ||::: ||::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1038 LeuPheAspAlaAlaGlyCysLeu-----ArgThrThrSerProGluAlaIle 1054
 Qy 320 ACT-----GAATAACTAAG 334
 Db 1055 ThrlGlnGluPheTyrAspSerArgGlnGluLysTyrValGlnArgLysGluIleIle 1074
 Qy 335 GCTGTGTTATACCTTAACCT-----CTTACGACATAATAACAAGTTACTTGGAAA 388
 :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1075 GlyValLeuGlnAlaGlnSerLysArgLeuThrAsnGlnAlaArgPheIleLeuAlaLys 1094
 Qy 389 ATGAATTCGAG-----GAGGAAGTGAAGTGGCAGGTGATCATCA 430
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1095 IleAsnAsnGluIleValLeuGluAsnLysLysLysAlaAlaIleValAspValLeuIle 1114
 Qy 431 GGAGCCGAGA-----GCTGAGATGACTTCGAAACACCCAGAGACTGAGCTGGAAC 484
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1115 LysMetLysPheAspAlaAspProValLeuGluGlnLysLeuIleGlu 1134
 Qy 485 ACTTGGATGACTCCGAGTGTGCTTCAGAGATGCCAGGAGA-----GCTGCATATCA 538
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 1135 -----LeuArgGluUserGlyIluIleGluLeuAspGluAspLeuAlaIaAlaValAla 1152
 Qy 539 ACTGGCCAGATCAGGCCTCTATAACGCCAGGATCACATCG----- 583
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1153 ValGluGluAspGluAlaAllecerSerAlaAlaAlaAlaAlaAlaAlaAlaAla 619
 Qy 584 -----CTGCTGAAACTGCAGGTGAGAGGTGACACAGCTC 619
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1173 TyrAspTyrLeuValGlyMetalAlaLeuIleIleGluUserGluGluGluLysLysIle 1192
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Qy 620 TCCCGAAAGCAGAACCAAGCTGCGCAGACAGATAGAGAGCCTCGAG-----CAG 673
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1193 IleLysGluUserGluGluLysMetAlaIagluValArgValIleGluLysLysIle 1231
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Qy 674 AAAACACAGGAGAAGGGAGAGCGGCTGACTCGGAG-----CAGGAGGCCCTAC 724
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1213 AspLeutPheIleGluAspLeuAspPheValSerGluLeuAspLysGlnGluAla 1231
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Qy 725 CTGCGCTGAGGATGAGGGCCTGAGCAACTGCCCCTGTCCTCCACTAGTGGGAAAGCA 784
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1232 ---ArgIle----- 1235
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Qy 785 GGGCAAGATGCCACCTGCCAGGGTGGCATGACAGTCGTCGCCCCGAGAGGGCCG 844
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1236 AspGluAspAlaSerIleLysAsnAlaAlaLysLysLeuAlaAlaAspAlaIysThrGly 1255
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Qy 845 AGTCCC-----TGCCCTGGCAATCAGGCCAG 871
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1256 ArgGlyProLysLysAsnValCysThrGluValLeuProSerIlyAspGlyGin 1273
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 RESULT 9
 WMBEH6
 UL36 protein - human herpesvirus 1 (strain 17)
 C;Species: human herpesvirus 1
 C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
 C;Accession: T30085
 R;McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.;
 J. Gen. Virol. 69, 1331-1354, 1988
 A;Title: The complete DNA sequence of the long unique region in the genome of herpes
 A;Reference number: A30083; MUID:88274327; PMID:283594
 A;Accession: T30085
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-3184 <MG>
 A;Cross-references: GB:X14112; NID:gi1944536; PIDN:CAA32311.1; PID:959536; GB:D00317
 C;Genetics:
 A;Gene: UL36
 C;Superfamily: varicella-zoster virus gene 22 protein
 Alignment Scores:
 Pred. No.: 1.47 Length: 3164
 Score: 106.50 Matches: 85
 Percent Similarity: 33.12% Conservative: 21
 Best Local Similarity: 26.56% Mismatches: 129
 Query Match: 4.41% Indels: 85
 DB: 1 Gaps: 17
 US-09-939-293-1 (1-1358) x WMBEH6 (1-3164)
 Qy 1252 CAGCTGCTCACAGGACAGTGGGGCAGATCA-----GAG 1217
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 2581 GluLeuIleAspAspPspSerGlyProAlaProLeuAlaProAspProLeuUser 2600
 Qy 1216 AACACATCAGAAATACATACAAAGAACATGTCAGAACCTGGACAGGAGTCGCCCCCTCCCTGC 1157
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 2601 ProThrAlaAspGlnSerValProThrSerGlnCysAlaProArgProProGlyProAl 2620
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Qy 1156 CACACT-----SGCATCAGACAGGACAGTCAATCATT 1115
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 2620 avalThrAlaArgGluAlaArgProGlyValProIaGluSerThrArgProAla----- 2638
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Qy 1114 TTGACGACGTTAAAGACTGAAACAGGTTAACAGTGTGCTGAACCTAAGGCATGAC 1055
 :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||

Db	2639	Best Local Similarity:	25.85%	Mismatches:	48
QY	1054 AAA--AGGACTCCCTCTCTGACCGAGGTAGCAATGCTTGTTGAGTAA 998	Indels:	29	Gaps:	6
Db	2647 gargleProserProglnSerSerProAlaProProAspAlaThrlalaProArgProPr 2667				
QY	997 AAAATGGTAGAGCAGCTGACAGAGTGGGGTGAAATGTAAACAGGGTGAGTGCACCA 938				
Db	2667 olaSerSerArgAla-----SerAlaSerSerAla-----SerAlaSerSer 2678				
QY	937 AGGGCTAGAACCCAGTCAGCAAGCCAGACAGAGGGACTCAGCTCACACA 878				
Db	2678 rAlaThrThrGlnGlyTrp-----ArgProProAlaLeu---ProAspThr 2713				
QY	817 CATGCCAACCCCTGGCAGGGTG--GCATGCGCCCTGCCCCTACTGAGTGGGAGA 761				
Db	2713 OHisAlaLeuValSerAspPheAlaArgProProAlaProProLysProGluAlaP 2733				
QY	877 AGGGCTCTCCGTATGGCCAGGGCAGGACTGCGCCCTCTGGGACACAGT 818				
Db	2698 rAlaThrThrGlnGlyTrp-----ArgProProAlaLeu---ProAspThr 2713				
QY	817 CATGCCAACCCCTGGCAGGGTG--GCATGCGCCCTGCCCCTACTGAGTGGGAGA 761				
Db	2713 OHisAlaLeuValSerAspPheAlaArgProProAlaProProLysProGluAlaP 2733				
QY	760 CAGGGCTGCTGGCAGGAGTG--GCATGCGCCCTGCCCCTACTGAGTGGGAGA 713				
Db	2733 OHisAlaLeuValSerAspPheAlaArgProProAlaProProLysProGluAlaP 2733				
QY	712 CTCCGACTCACGCCGCTCCCTCCCTGCTGTTCTCACGGAGCCTCTATCG 653				
Db	2753 erProAlaLeuProLysAspProAlaProProAlaProAlaProAla 2769				
QY	652 TGCTCTGCTGAGCTGGTT-----CTGCTTCGGGAGCTGGTGGCAC 608				
Db	2769 hrValLeuProGlyGlyLysAsnArgArgProProLeuThrSerGly----ProAlaP 2787				
QY	607 CTCTCTACCTGAGCAGTCACAGCTGAATGATTCCTGGGTATAGAGGCUGATC 548				
Db	2787 roThrProProArgVal--ProValGlyGlyProGlnArgLeuThrArgPro--- 2804				
QY	547 TGGCCGAGTTGATATCCAGCTCTCTGCAAGACCACTGAGCTCA--- 492				
Db	2805 -----AlaValAlaSerLeuSerGluSerArgGluSerIleP 2817				
QY	491 --TCCAGTAGGTTTCCAGCTCAAGACTCTCTGCTGTTG----- 453				
Db	2817 roSerProTrpAspProAlaAspProThrAlaProValLeuGlyArgAsnProAlaGluP 2837				
QY	452 --AAGCATCTCAGCTGGCTCTATGATCACCTGGCACACTTCATCTCTCTCT 399				
Db	2837 roThrSerSer-----SerProAlaGlyProSerProProPro 2849				
RESULT	10				
G02520	plectin - human				
C;Species:	Homo sapiens (man)				
C;Date:	20-Jun-1997 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999				
C;Accession:	G02520				
R;McLean, W.H.I.; Smith, F.J.D.					
A;Reference number:	H01385				
A;Status: Preliminary:	submitted to the EMBL Data Library, March 1996				
A;Accession:	G02520				
A;Experimental source:	GB/EMBL/DDJB				
A;Cross-references:	EMBL:U53204; NID:91477645; PID:AAB05427.1; PID:91477646				
A;Gene:	PLEC1				
C;Superfamily:	plectin; alpha-actinin actin-binding domain homology; ribosomal protein S				
F;68-283/domain: alpha-actinin actin-binding domain homology <ACT>					
Alignment Scores:					
Pred. No.:	1.84	Length:	4574		
Score:	105.50	Matches:	38		
Percent Similarity:	47.62%	Conservative:	32		
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
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Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
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QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
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QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
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QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
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QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
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QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
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Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
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Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
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QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
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QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTGAGGACCCAGTAACACTCTGACCCCTCTCTAGTAGATAAGTTTCA 1264				
Db	55 LeuPheAlaGlyAlaProAspAlaHisSerAlaSerPhe----- 66				
QY	1263 CTCTCTGCGCTCAGCTGCTCTCACAGGACAGTGGGGAGATCAGAGAACACATCTCAGAA 1204				
QY	1323 CTCCTG				

ALIGNMENT

REFERENCE DOCKET NUMBER: 8600-0177.30
 TELECOMMUNICATION INFORMATION:
 TELPHONE: 650-324-0880
 TELEFAX: 650-324-0960
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 591 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal

US-08-965-903B-2

Alignment Scores:
 Pred. No.: 0.0432 Length: 591
 Score: 106.00 Matches: 74
 Percent Similarity: 34.86% Conservative: 40
 Best Local Similarity: 22.63% Mismatches: 115
 Query Match: 4.33% Indels: 98
 DB: 3 Gaps: 16

US-09-939-293-1 (1-1358) x US-08-965-903B-2 (1-591)

QY 518 GCAGCGAAAGGTGCAATCAACTGGCCAGATCAGGCCCTATAACGCCAGGATCAC 577
 Db 209 AlaThrArgSerGlnHisProLysProlaGlyLysGlnAspGlnAlaSer 228

QY 578 ATTCACTGGCAAACTGCAAGTGGCAACTGGCAGGGGAGGTCACAGCAGCTCTCCGGAAAGCAGAAC 637
 Db 229 LeuLeuLeuLeuProGlnArgAspGlnHisLeuHis--LeuGlnGlnHisGlnLeu 247

QY 638 AAGCTGCAGAGCAGAGATAAGAGCTGGTAGAGAGGCTGGTAGAAACACAGGAGGGAGGAG 697
 Db 248 LeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 267

QY 698 CGGGCTGAGTCGGACAGGAGGCCACTG-----CGTAGGATTGAGG 742
 Db 268 HisGlnGlnAsnGlnGlnHisAlaArgLeuAlaThrThrGlnAlaThrSerValGly 287

QY 743 CCTGACACACTGCCGTCTCCCACTCA-----GtGGGAA 781
 Db 288 SerAspHisthAspGlyLeuLeuHisSerHistLeuGlnAsnSerThrThrLysProPro 307

QY 782 GCAGGGCAGATGCCACCCAGGGTGGCATGACTCTCTGCAACGGAGAGGCC 841
 Db 308 AlaSerLysGlnProLalaLeuProArgLeuGlyMetGlyLysLeu-----Gly 322

QY 842 GGCAGCT-----CCGCCCGGCCAA 862
 Db 323 -LeuGlyLeuGlyLeuGlyLeuAsnGlnProleLeuLeuGlnProLysGlnProThrProAla 342

QY 863 TCAGGGAGAGCCCTTGAGCTGAGCTGAGTCCTCTGGCTCAGGCTGGCTGGAC 922
 Db 342 rGlnLysGluArgMetHisAlaLeu-GluGluLeuLeuGlnProGlyGlyAlaGlyGlyA 362

QY 923 CTGGCTTAAGCCCTGGGACTCTGCA-----CCCTGTTAACATTCTACCCCACTCTG- 975
 Db 362 snglyGly--ProLeuValMetalAlaGlyAspProSerLeu--LeuAsnProLevalc 380

QY 976 -----TACAGCTGCTTAACCCATTTTTACCTACA 1009
 Db 380 ysPROArgCysGlyArgCysArgCysLysCysGlnCysGlnSerProArgProLeuProGln- 399

QY 1010 CCCAAGCATTGCTTACCTGGCTAGAGGAGGCTCTTGTCTGCC----- 1062
 Db 400 -----ThrTrpAlaCysAsnLysThrCysSerAlaGluSer 414

QY 1063 -CTPArgTCAGCACTGTTAACCTGTTCTGCTCTATTACGGTCGTCAAAATGAT 1120
 Db 414 alileAspTyrAlaSerCysLeuCysCysCysAlaLeu-----P 428

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/030232

FILED DATE: 07-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Petitionary, Joanne R

REGISTRATION NUMBER: 44,995

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/965,903B

FILED DATE: 07-NOV-1997

CATEGORY: Classification: 435

QY 1121 TTGACTCTGTCTCCCTCTGTGGATGCCAGTGTGGCAGGGGGACCTGTCAG 1180
Db 428 hetYrhiscysalaArgasparAspLeuAspCysAspAspGlyAsnGlyThrProCysV 448
QY 1181 TT-----TGTAGATTCTTGAT----- 1200
Db 448 alAspAsnProCysSerCysGlyProTyrLysArgThrGlnArgTrpGlyTyrProGly 468
QY 1201 -----GTTTCGATG-----TGTCTCTGA 1222
Db 468 laLeuSerIlePheLeuProCysLeuTrpPheTyTrpProMetArgGlyCysMetLysL 488
QY 1223 TCTGCCCACTGTCTGTGAGCACAGCTGAGGAGTGAACAAACCTTACT 1282
Db 488 euCysCysLysCysTyrGlyArgPheAla----- 497
QY 1283 AAGAGAAGGGGTGCGA 1299
Db 498 --GlyArgGlyCysArg 502

RESULT 3

; Sequence 12, Application US/08660963

; Patent No. 5852187

GENERAL INFORMATION:

APPLICANT: Thorner, Michael O.

APPLICANT: Gaylinn, Bruce D.

APPLICANT: Horikawa, Reiko

APPLICANT: Lyons Jr., Charles E.

TITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY GROWTH HORMONE-RELEASING HORMONE RECEPTOR

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: POHLM, HAIK, SCHOBREICH & KAUFMAN, LTD.

STREET: Metropolitan Square Building, Suite 800, 1450 G. Street

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patientin Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/660,963

FILING DATE: 12-JUN-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: O Shaughnessy, Brian P.

REGISTRATION NUMBER: 32,747

REFERENCE/DOCKET NUMBER: 18046.036

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-824-8000

TELEFAX: 202-824-8199

TELEX: 24816

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 498 amino acids

TYPE: amino acid

STRANDEDNESS: linear

TOPOLOGY: protein

MOLECULE TYPE: protein

US-08-660-963-12

Alignment Scores:

Pred. No.: 0.0448 length: 498

Score: 105.50 matches: 93

Percent Similarity: 33.15% conservative: 28

Best Local Similarity: 25.48% mismatches: 102

Query Match: 4.37% indels: 142

Gaps: 23

US-09-939-293-1 (1-1358) x US-08-660-963-12 (1-498)

QY 1265 CACTCTTGSCCTCACCTGTCCTCACAGACAGTGGGGCATGAGAACATCAGA 1206
Db 21 HisGluLeuAla--AlaValThrThrGly AspGlyGlyArgSerThrGlyProProAr 39
QY 1205 AATACATACAN-----AGAAATGTCACAACTGGACA-----GGTRCCCCTC 1164
Db 39 gIeu-thRgInAlaLaJavalAlaGluLeuProProTrpProAlaAlaGlyCysGlyAlaPro 59

QY 1163 CCCCTCCACACTGGCATCCACAGA-----GGCACAGTCAAACTT 1113
Db 59 laserSerAlaCystPheLeuProCysGlnSerTrpAlaThrCysSerValM 79

QY 1112 TGACGAGCTAATAAGACTGAAACAGGTTAACACTTGTGACTTAAGGCATCACAA 1053
Db 79 etSerSer--LeuSerGluGlySerIlyShistAlaTyrLysIleLeuLysGlyCysP 98

QY 1052 AAAGGACTCTCTGCTGACCCAGTAGGCAAATGCTTGGTGTGAGGTTAAAATAA 993
Db 98 rothrProProTrpPheAlaProGly-----SerglythGlyCysCysAlaGlyArg 116

QY 992 GGTAAGAGCAGCTGACAGTGG-----GTGAATGTAACAGGT 948
Db 116 rp-----GlnAlaLeuGluSerGlyAlaSerProAlaArgLeuSerSerLeuThrSerA 134

QY 947 GCAGTCCCAAGGCTAAAGA-----ACCAGTCCAGCGGAAGCC 909
Db 134 latProSerGlySerArgLysLeuArgLysAlaProLeuGlnAlaGlyArgSerProSerArgL 154

QY 908 TGAGACCAAGGAGGACT-----ACAGGTCACA 879
Db 154 euileProAlaLeuCysProTrpSerCysLeuArgArgAsnProThrProAla 174

QY 878 AAGGCTCTCG-----CCTGATTGSCAGGGCAGG 849
Db 174 rglySerSerThrProTrpAlaThrAlaSerArgLeuGlnProSerTrpProSerS 194

QY 848 AC-----CTGC 843

Db 194 extrpSerLeuSerGlySerThrAlaProGlyThrSerThrProSerCysSerP 214

QY 842 CGCTCTCTGGTGACAGACAGTCATGC-----CAA 810
Db 214 roProLeu-SerSerArgArgLysLeuCysSerArgThrProSerPheThrGlyArg 233

QY 809 CCCTGGCAAGGGCATCTGCCCCGCTCTTCCCCCTGACTGGGGAGAAGGGAGTGT 750
Db 234 ThrTrpThr-----ThraLaAlaSerProLeu-----Cys 244

QY 749 GCTCAGCCCTCAATCTCAGCAGTAGGCTCTCCGCTCC-----708

Db 245 AlaArgLeuLeuProProLeuLeuSerArgProProSerAlaGlyCysTrpGlnLys 264

QY 659 CTATCCTGCTCTGCCAGCTGATGTTCTGTTTCTGGGAGAGCTGGTGCACCTCTCCA 600
Db 285 LeuCysThrProAlaSerProLeuProHisCysProAlaGlyGlySerGlyGlyTrp 284

QY 659 CTATCCTGCTCTGCCAGCTGATGTTCTGTTTCTGGGAGAGCTGGTGCACCTCTCCA 600
Db 285 PheSer-----LeuProGlyGlyPheLeuCysSer----- 294

QY 599 CCTGCCACTTCACCACTGATGTTCTGTTTCTGGGAGAGCTGGTGCACCTCTCCA 600
Db 295 -----SerProLysCysGlySerValAlaSerProLeu----- 306

QY 548 CTGGCCAGTTGATATGAGCTCTGCTGCCATCTGAAAGACCAACTGCAGTCATCC 489
Db 307 -----LysLeuArgAlaGly 312

QY 488 AAGTGGTT-----CCAGCTCAGTCTCT 462

RESULT 4

US-08-882-046-5
; Sequence 5, Application US/088882046
; Patent No. 6136952
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; APPLICANT: Hood, Leroy
; APPLICANT: Kranz, Ian D.
; APPLICANT: Spinner, Nancy B.
; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08-882-046
FILING DATE: 25-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Kathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-FW-2637

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9901
TELEFAX: (619) 535-8949

INFORMATION FOR SBO ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1219 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-882-046-5

Alignment Scores:

Pred. No.	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
481	104.50	1219	71	37	131	125	19

US-09-939-293-1 (1-1358) x US-08-882-046-5 (1-1219)

QY 481 AACCACTTGATGACTCGCAGTTGGTGT----- 507

Db 666 AsnAsnIleasnAspCysSerGlnAsnProCysHsTyrglyGlyThrCysArgAspLeu 685

QY 508 TTCAAGATGATGCCAGCAGACTGCATTCAACTGGCCAGATCAGGCCCTATAACCGC 567

Db 686 ValAsnAspPheTyrcySAspCysLysAsnGlyTrpLysLysHsSerArg 705

QY 568 CAGGAATCACATTCACTGGAACTGCAAGTCAGGAGGAGCAGCTCCCGAA 627

Db 706 AspSer---GlnCysAspGluAlaThrCysAsnAsnGlyGlyThrcySystyAspGlu 723

QY 628 -----AGCAGAACCAAGCT 642

RESULT 5

US-09-308-022-6
; Sequence 6, Application US/09308022
; Patent No. 6291554
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF MINNESOTA, ET AL.
; TITLE OF INVENTION: C3 BINDING PROTEIN OF STREPTOCOCCUS
; TITLE OF INVENTION: PNEUMONIAE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.

Db 744 ArgAsnSerSerCysLeuProAsnProCysHsAsnGly----- 757

Db 703 TGAGTCGGAGCAGGGCCCTACTCGTGAGGATTAGGGCTCAGCACACTGCCCTGTC 762

Db 758 ----- 761

Db 823 CTGAGCACCAGAGAGGGCAGGCCAGGCTGCCAGGCC 861

QY 763 TCCCCACTCAGTGGAAAGCAGGGCAGATGCCACCCCTGCCAGGGCTGGCATGACTCT 822

Db 778 IleCystThrGlnAsnThrAsnAspCysSerProHisProCysTyraSerGlyThrCys 797

Db 762 -----AsnGlyAspSer---PheThrCysValCysLysGluGlyTyrPheGluGlyPro 777

QY 862 ATAGGGCAGACGCCCTGAGCTGAGTGCCTCTGGCTCTAGCTTGCCGTGGA 921

Db 798 ValAspGlyAspAsnTrpPheArgCysGluCys-----AlaProGlyPheAlaGly 814

QY 922 CCT----GGTCTTAGCCCTGGCACTGACCCGTTAACATTCACCC 969

Db 815 ProAspCysArgIleAsnIleAsnGlyCysGlnSerSerProCys---AlaPheGlyAla 833

QY 970 ACTCTG-----TACAGCTGCCCTTACCCATTTCATGCCCTTAAGTC 1011

Db 834 ThrCysValAspGluIleAsnGlyTyrGlnCysIleCysPro----- 847

QY 1012 CAAGCAGATTGCCACCTGGTCAGAGAGGAGGCCCTTGTCTATGCCCTTAAGTC 1071

Db 848 -----ProGlyHisSerGlyAlaLysCysHsGluValSerGly 860

QY 1072 AGCAACTGTTAACCTGTTCACTCTATTAGCTGTCGCAAATGATTAGTAGTACTGT 1131

Db 861 ArgSerCysIleThrMetGlyArgValIleLeuAspGlyAlaLysTrpAspAspCys 880

QY 1132 TCCCTCTG-----TGGATGCCAGTGT 1155

Db 881 AsnThrCysGlnCysLeuAsnGlyArgValAlaCysSerLysValTrp-----Cys 897

QY 1156 GGC-----AGGGGAGGGAACTGTCCA----- 1179

Db 898 GlyProArgProCysArgIleUhiLysGlyHsGluCysProAsnGlyGlnSerCys 917

QY 1180 GTGTGTTACATTCTTGTATGTTCTGATGTTGTCCTGTGATCTGCCCTACTG----- 1236

Db 918 IleProValIleLeuAspAspGlnCysPheAlaLysProCysThrGlyAlaGlyGlyCysArg 937

QY 1237 -----CCNGTGGAGCACGCTGAGGCCAAGGAGTGAAGAAACCTATTCATC 1281

Db 938 SerSerSerLeuGlnProValLysThrLysCysThrSerAsp----SerTytyr--- 954

QY 1282 TAAGAGAAGGGTCCAGAGCTTACCTGGTGTCTCACAGGACTAACATCACAGGA 1341

Db 955 --GlnAspAspCysAlaAsnIleThrPheThrPheAsnLysGluMetMetSerProGly 973

QY 1342 CTTAACACAGAA 1353

Db 974 LeuThrThrGlu 977

STREET: 119 No. 6291654th Fourth Street, Suite 203
 CITY: Minneapolis
 STATE: Minnesota
 COUNTRY: USA
 ZIP: 55401

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/308,022
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/20586
 FILING DATE: 12-NOV-1997
 APPLICATION NUMBER: 60/029,444
 FILING DATE: 12-NOV-1996
 APPLICATION NUMBER: 60/038,086
 FILING DATE: 18-FEB-1997
 APPLICATION NUMBER: 60/059,368
 FILING DATE: 19-SEP-1997
 APPLICATION NUMBER: 60/062,473
 FILING DATE: 16-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: MOTTING, ANN M.
 REGISTRATION NUMBER: 33,977
 REFERENCE/DOCKET NUMBER: 110.00430101
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-305-1228
 TELEFAX: 612-305-1228
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 564 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-308-022-6

Alignment Scores:
 Pred. No.: 0.168
 Score: 100.00
 Percent Similarity: 37.75%
 Best Local Similarity: 19.54%
 Query Match: 4.09%
 DB: 4
 Gaps: 8

US-09-939-293-1 (1-1358) x US-09-308-022-6 (1-564)

Qy 167 TTGGAGTAACCTGTCGCGGTCTATGCA-----CAGAACATCAGAGCTCATR 217
 ||| :::: :::: :::: ::||| :::: ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| 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::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| 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::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||

Db 110 LysSerLysaspGluLeuProSerGluile-----lysAlaLysLeuaspAlaala 126
 Qy 458 CACCAGAAGTACTTGAGCTGGAACCACTTGATGACTGCTGCAGATG 517
 Db 127 PheGluLysPheLysLysaspThrLeuLysProGlyLysValAlaLysLys 146
 Qy 518 GCAGCAGAGCTGCATATAACGCCCTATAACGCCAGATCAGCTCC 577
 Db 147 LysValGluLysLysLysAlaLysaspGlnLysGluLysaspGargAsnTyr 166
 Qy 577 ----- 577
 Db 167 ProThrAsnThrTyrlsThrLeuGluLeuGluLeuAlaLysPheAspValLysVal 186
 Qy 578 -----AntCAsCTGGTCAACGCTGCAAGCTGGAGAG-----GRC 610
 Db 187 GluAlaLysLeuGluLeuValAlaLysGluLysLysGluSerArgAsnGluGlyThrIle 206
 Qy 611 CACCACTCTCCGGAAACCACTGGCAGAGCACAGTAGAAGAGCTCC 670
 Db 207 LysGlnLysLysGluLysValGluLysLysProGlyLysValAlaLysArgLysGluLys 226
 Qy 671 CAGAAACACAGGAGGGAGGGCTGAGCTGGAGCAGGCACGGCTACCGCT 730
 Db 227 LysThrAspArgLysLysAlaLysGluLysLysArgLysValAlaLysAspAlaLysLeuLys 246
 Qy 731 GAGGATTGAGGCCCTGAGCACACTGCCGCTCCACCTCAGIGGGAAAGCAGGGCA 790
 Db 247 Glu-----AlaAsnValAlaThrSerAspGlnGlyLysProLysGlyArgGluLys 262
 Qy 791 GATGCCACCTGCCAGGGTTGGCATGACTCTGTCGACCGAGAGAGGGGGCAGTC 850
 Db 263 LysArgGlyValProLysGluAsnValAspAlaLysSer 282
 Qy 851 TGCCCCTGGCCATCAGGGAGACGCCCTGTGAGCTGCTGAGCTGCTGAGTC 910
 Db 283 SerAspSerServerGlyGluGluThrLeuProSerSerSerLeuLysSerGlyLys 302
 Qy 911 CTGGC 916
 Db 303 ValAla 304

RESULT 6
 US-08-231-193A-54
 Sequence 54 Application US/08231193A
 Patent No. 5849895

GENERAL INFORMATION:

APPLICANT: DAGgett, Lorrie P.
 APPLICANT: Ellis, Steven B.
 APPLICANT: Liaw, Chen W.

INVENTOR: Lu, Chin-Chun

TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
 NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1610 Union Street
 CITY: San Diego
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92101-2226

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOSE/MS-DOS
 SOFTWARE: Patent In Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/231,193A
 FILING DATE: 20-APR-1994
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/052,459
 FILING DATE: 20-APR-1993

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08/480,474
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
 NAME: Sedman, Stephanie
 REFERENCE/DOCKET NUMBER: 33-779
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-238-0999
 TELEFAX: 619-238-0062

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1214 amino acids
 TOPOLogy: amino acid
 MOLECULE TYPE: protein

US-08-480-474-54

Alignment scores:
 Pred. No.: 0.375 Length: 1214
 Score: 98.00 Matches: 65
 Percent Similarity: 33.58% Conservative: 25
 Best Local Similarity: 24.25% Mismatches: 92
 Query Match: 4.06% Indels: 86
 DB: 3 Gaps: 12

US-09-939-293-1 (1-1358) x US-08-480-474-54 (1-1214)

QY 1009 TGTGAGCTTAAATGGTAGAGCAGCTG----- 977
 Db 913 CysProThrProArgSerGlyLysLeuProAlaCysAlaArgP 1089

QY 976 -----ACAGAGTTGGTGAATGTTAACAGGGTCAGTGCCAAAGGCTAACAGAC 926

Db 933 ProSerProThrGlyTrpG----- 939.

QY 925 CAGGTCCAGGCGCAAGGCTGAGCACACAGGAGCACTCACAGCTCACAAAGGGCTCGCC 866

Db 940 -----ProproAsp-----GlyGlyArgAlaAlaLeuValArgAlaP 953

QY 865 TGATTCGCAGGCCAGACCTCCGCTCTTGATCACGCCACCTC 806

Db 953 ocnInProProGlyArg-----ProProAspProPro-----LeuSerAspVa 969

QY 805 GGCAGGGGGATCAGCCCTCTGGTGCAGACGTCAGTCAGCCACCT 752

Db 1049 snalaAlaLtrPalaArgGlySerArgProSerHisAlaSerLeuProSerValAlaG 1069

QY 587 -----CCTCACCCAGGAGCTCCACTGAGCTGCTGGGTATAAGGC 554

Db 1069 luAlaPheAlaArgProSerSerLeuProAlaLysLeuProAlaCysAlaArgP 1089

QY 553 CTGAT-----CTGGCCAGTTGATGCACTCTGCTGCCAT 515

Db 1089 roASPGlyHisserAlaCysArgArgLeuAlaGln-----AlaGlnSerMetCysLeuPro 1108

QY 514 CTCAGAAGACCAACTCGAGTCATCCAAAGTGGTTCCAGCTCAAGT----- 468

Db 1108 leTyraRgGluaLcAlysGlnGluGlyGluGlnAlaGlyAlaProAlaLtrPglnHiSArg 1128

QY 467 --ACTCTGGTTGGAGCTCATCAGCTGGCTCTTGATCACGCCACCTC 410

Db 1128 InhiValValCysLeuHiSAlaHiSAlaHiSLeuProLeuCysTrpGlyAlaValCysProH 1148

QY 409 ATCTCTCTCTCTGAACTCA 390

Db 1148 IsleuProProCysAspSer 1154

RESULT 8

US-08-480-474-54

Sequence 54, Application US/08480474

Patent No. 6038865

GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie P.
 APPLICANT: Ellis, Steven B.
 APPLICANT: Liaw, Chen W.

APPLICANT: Lu, Chin-Chun

APPLICANT: Niu, Ming-Chang

TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: CA

COUNTRY: U.S.A.
 ZIP: 92101-2026

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

SEQUENCE CHARACTERISTICS:
 LENGTH: 1219 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-231-193A-50

Alignment Scores:
 Pred. No.: 0 376
 Score: 98.00
 Percent Similarity: 33.58%
 Best Local Similarity: 24.25%
 Query Match: 4.06%
 Gaps: 12

US-09-939-293-1 (1-1358) x US-08-231-193A-50 (1-1219)

QY 734 ----CCTCACGGCAGCTAGGCCCTCGCTCGACTCAGCCGCCTCCCTCCCTCG 680
 ||||| ||||| ||||| ||||| |||||
 Db 1009 erpheproargalaaspargsergylargpropheleuproleupheprogluipro 1029

QY 679 TGTWTCTGACGGGACTCTCTTA-----TCTGAGCTTC 647
 ||||| ||||| |||||
 Db 1029 luleugluaspgleuproleuleuglyprogluglnleualargarggluialeuleu 1049

QY 646 TGCCACCTGGTTCTGCTTCGGAGACCTGGCACCTCTCCACCTGGAGCTTC- 588
 ||||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1049 snAlaAlaLtpalaarglysergylargProSerHsAlaserLeuproSerServAla 1069

QY 587 -----CCAGCTGAAATGTTGATTCCTGGGGTATAGAGG 554
 ||||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1069 lualaphealaargproserserleuproAlaGlycystriplglyproAlaCysalaArgP 1089

QY 553 CTGAT-----CTGGCCACTTGATATGATCAGCTCTGCAT 515
 ||||| ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1089 roAspGlyHisserAlaCysargargleuAlaGln--AlaGlnSerMetCysLeupro 1108

QY 514 CTCGAAAGACCAACTGCACTCATCCAAAGTGTTCAGCTTCAGT 468
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1108 letyrargGluaLacysglulglygluAlaProAlaLtprglnHisArg 1128

QY 467 --ACRTCTGGTTGAAGTCATCTCAGCTCTGGCTCTATGATCACCTGCCACACTC 410
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1128 InHisvalCysleuHisAlaHisleuProleuCystriplglyAlaValCysProH 1148

QY 409 ATCTCTCCCTGATTC 390
 ||||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1148 isLeuproProCysasPser 1154

RESULT 13
 US-08-231-193A-50
 ; Sequence 50, Application US/08231193A
 ; Patent No. 5549895

GENERAL INFORMATION:
 APPLICANT: Daiggett, Lorrie P.
 APPLICANT: Ellis, Steven B.
 APPLICANT: Liaw, Chen W.
 APPLICANT: Lu, Chin-Chun

TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
 TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
 NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92101-2926

COMPUTER READABLE FORM:
 COMPUTER TYPE: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatientInRelease #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/231,193A
 FILING DATE: 20-APR-1994
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/052,459
 FILING DATE: 20-APR-1993
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-9383
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-238-0999
 TELEFAX: 619-238-0062

INFORMATION FOR SEQ ID NO: 50:

QY 1009 TGTGAGGTTAAAAATGGGTAAGGCCAGCTG 977
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 918 CysProThrProArgSerGlyProSerProCysLeuproThrProAspProProProGlu 937

QY 976 -----ACAGAGTGGGTGAATGTTAACAGGGTGAGTGGCCAAAGGCTRAAAC 926
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 938 ProSerProThrGlyProGly----- 944

QY 925 CAGGTCAGGCCAACGCTGAGACCACAGGAGCCTCACCTCACAAAGCGCTCGCC 866
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 945 -----ProProAsp-----GlyGlyArgGalaLaleuValLargArg-AlaPr 958

QY 865 TGATRGCCAGGGCAGGCCACCTGCGCTCTCGTGTGACAGACAGTCAGGCCAACCT 806
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 958 oGlnProProGlyArg-----ProProAspPro-----ProProGlyPro-----LeuUserAspVa 974

QY 805 GGGCAGGGTSCATCGCCCTGCTTCCTCCACTGAGTGGGAG-----ACAGGGACT 752
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 974 IserArgValSerArgProAlaLtprglnHisArgProAlaLtprglnHisArg 994

QY 751 GTGCTCAGGCCCTCAAT----- 735
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 994 YsGlyArgHisleuSerAlaSerGluArgProleuUserProAlaArgCysHistyrsS 1014

QY 734 ----CCTCACGGTAGGCTCCCTGCTCGACTCAGGCCGCCTCTCCCTCTCTCG 680
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1014 erpheproargalaaspargsergylargPropheleuproleupheprogluipro 1034

QY 679 TGTWTCTGACGGACTCTTA-----TCTGAGCTTC 647
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1034 luleugluaspgleuproleuleuglyprogluglnleualargarggluialeu 1054

QY 646 TGCCACCTGGTTCTGCTTCGGAGAGCTGGTCCACCTTCACCTGCCAGTTCA- 588
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1054 snAlaAlaLtpalaarglysergylargProSerHsAlaserLeuproSerServAla 1074

QY 587 -----CACTGAAATGTTGATTCCTGGGCTATAGAGG 554
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1074 lualaphealaargProserSerLeuproAlaGlycystriplglyproAlaCysalaArgP 1094

QY 553 CTGAT-----CTGGCCACGTTGATGAGCTCTGGCGCAT 515
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1094 roAspGlyHisserAlaCysargargleuAlaGln--AlaGlnSerMetCysLeupro 1113

QY 467 --ACRTCTGGTTGAAGTCATCCAGTGTTCAGCTTCAGT 410
 ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1133 InHisvalCysleuHisAlaHisleuProleuCystriplglyAlaProAlaLtprglnHisArg 1153

QY 409 ATCTCTCCCTGATTC 390
 ||||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
 Db 1153 isLeuproProCysasPser 1159

RESULT 14
 US-08-486-273A-50
 ; Sequence 50, Application US/08486273A
 ; Patent No. 598586
 ; GENERAL INFORMATION:
 ; APPLICANT: Daggett, Lorrie P.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Law, Chen W.
 ; APPLICANT: Lu, Chin-Chun
 ; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,273A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-9383B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-238-0999
 TELEFAX: 619-238-0062
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1219 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-486-273A-50
 Alignment Scores:
 Pred. No.: 0.376
 Score: 98.00
 Percent Similarity: 33.58%
 Best Local Similarity: 24.25%
 Query Match: 4.06%
 DB: 2
 Length: 1219
 Matches: 65
 Conservative: 25
 Mismatches: 92
 Indels: 86
 Gaps: 12
 US-09-939-293-1 (1-1358) x US-08-486-273A-50 (1-1219)
 OY 1009 TGTGAGGTAAAAAAATGGTAAAGCAGCTGT----- 977
 Db 918 CysProSerProArgSerGlyProSerProCysLeuProThrProAspProProProGlu 937
 QY 925 CAGGCCAGGCAGCCAGCTGAGACCACTCACGCTACAAGGCGTCGCC 866
 QY 945 -----ProProAsp-----GlyGlyLysGalaAlaLeuValArgArg-AlaP 958
 OY 865 TGAATGGCAGGGCAGGACCTGGCCCTCTCTGGTSCACAGCATGGCAACCT 806
 Db 958 OGNProProGlyArg----ProProThrProGlyProPro----LeuSerAspA 974

QY 805 GGGCAGGGGCACTGCCCCCTGCCTTCCCACITGAGTGGGGAG----ACAGGGCAGT 752
 Db 974 1sErargvalserargargroalatrpgrlalargrp-ProvalargThrGlyHis 994
 QY 751 GTGCCTAGGCCCTCAT----- 735
 Db 994 ysglyarglisleuserasergluargproleuserpProAlaArgCysHistYrs 1014
 QY 734 ----CCTCACGGCAGGTGAGCTGGCTCTGCTCCGACTGAGCCTGCTCCCTG 680
 Db 1034 luLeugluaspleuProleuLeuGlyProGluGlnLeuAlaArgGluAlaLeu 1054
 QY 646 TGCCACGCTGGTTCTGCTTCCGGAGACTGGCACCTCTGCCACCTGCGATTCA- 588
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 QY 587 -----CCAGCTGATGCTATTCTGGCGTTATAGAGGC 554
 Db 1074 luAlaPheAlaArgProSerSerLeuProAlaLgylcysGlyProAlaLysAlaArgP 1094
 QY 553 CTGAT-----CTGCCCACTTGATATGACGCTCTGCTGCCAT 515
 Db 1094 roAspGlyHisSerAlaCysArgArgLysAlaGin---AlaInSerNetCysLeuPro 1113
 QY 514 CTCTGAAGACCAACTGCACTCATCCAAAGGGTTCCAGCTTCAGT----- 468
 Db 1113 letYArgGluAlaCysGlyGluGlyLysAlaProAlaLtpGlnHisArg 1133
 QY 467 --ACTCTCTCTCTGATTCATCTGCTCTGCTCTATGATCACCTGCCAACATTC 410-
 Db 1133 lnHISValCysLeuHisAlaHisAlaHisAlaLysLeuProAlaLysPro 1153
 QY 409 ATCTCTCTCTGATTCATCTGCTCTGCTCTATGATCACCTGCCAACATTC 410-
 Db 1153 lsLeuProProCysAspSer 1159

RESULT 15
 US-08-480-474-50
 Sequence 50, Application US/08480474
 Patent No. 6033865
 GENERAL INFORMATION:
 APPLICANT: Daggett, Lorrie P.
 APPLICANT: Ellis, Steven B.
 APPLICANT: Law, Chen W.
 APPLICANT: Lu, Chin-Chun
 TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING
 TITLE OF INVENTION: SAME AND USES THEREFOR
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,474
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-9382B

TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 1219 amino acids
TYPE: amino acid
TOPOLOGY: linear
NOT SOURCE: environmental

Db 1153 isleuproProCysAspser 1159 ||||||| : ::|||
Search completed: February 20, 2003, 15:03:39
Job time : 36.5 secs

	Alignment Scores:	Length:
pred. No.:	0.376	Matches:
Score:	98.00	Conservative:
Percent Similarity:	33.58%	Mismatches:
best Local Similarity:	24.25%	Indels:
Query Match:	4.06%	Gaps:
DB:	3	12
US-09-939-293-1 (1-1358) x US-08-480-474-50 (1-1219)		
QY 1009 TGTGAGGTAAAAAAATGGTAAGGACGCTGT-----	977	
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Db 918 CysProThrProArgSerGlyProSerProCysLeuProThrProAspProProProGlu 937		
QY 976 -----ACAGAGTGGGTGAATGTAAACAGGTGCAAGTGTCAAAGGTCAAAGGCTAAAGAAC 926		
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Db 938 ProSerProThrGlyLyrTpGly-----	944	
QY 925 CAGGCCAGCGCAAGCTGAGACCCACAGGAGGACTCACAGCTACAAGGGCTCGCC 866		
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Db 945 -----ProProAsp-----DProAsp-----DProAsp-----DProAsp----- 958		
QY 865 TGATGGCCAGGGAGGACCTGCAGCTCTCTCGTCAGACAGACAGTCATGCCAACCT 806		
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Db 958 GlnInProProGlyArg-----ProProThrProGlyProPro-----LeuSerAspVa 974		
QY 805 GGCAGGGTTGGCTCTGCCCTGCTTCCCACACTGAGTGGGAG-----ACAGGCACT 752		
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Db 974 ISeRArgValSerArgArgProAlaTrpLluAlaArgTrp-ProValArgThrGlyHisC 994		
QY 751 GRCCTCAGGCCCTCAAT-----	735	
Db 994 YSGLYIAGQHISleuSerAlaSerGluArgProLeuSerProAlaArgCysHistySerS 1014		
QY 734 -----CCCTCACCGAGTAGCTGCCCTCTGCTCCGACTCAGCCGCTCTCCCTTCCCTTG 680		
:::: :::: :::: :::: ::::		
Db 1014 eRpheProArgAlaAspArgSerGlyArgProheLeuProLeupheProGluProPro 1034		
QY 679 TGTGTTTCUGACGGAGCTCTCA-----		
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Db 1034 IuLeuGluLysPleuProLeuLeuGlyProGluGluIuLeuAlaArgArgGluAlaLeuAla 1054		
QY 646 TGCAGCTGGTTCTGCCTTCGGAGGCTGGCACCTCTCACCTGAGTCATCA----- 588		
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Db 1054 snlAlaAlaTrpAlaArgGlySerArgProSerHisAlaSerLeuProSerSerValAla 1074		
QY 587 -----CCGCTGAATGATTCCTGGGGTTATAGAGGC 554		
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Db 1074 IuAlaPheAlaArgProSerSerLeuProAlaGlyCysThrGlyProAlaCysAlaArgP 1094		
QY 553 CTGAT-----		
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Db 1094 roaspGlyHiSerAlaCysSargArgLeuAlaLagIn--AlaGlnSerMetCysLeuPro 1113		
QY 514 CTCGAANGACCACACTGCAGTCATCCAATGGTTTCAGCTTCAGT----- 468		
:::: :::: :::: :::: ::::		
Db 1113 leTyraGlyAlaCysGlyGluLysGlyLysAlaGlyAlaProAlaLtrPglnHiSArgG 1133		
QY 467 - ACTCTGGTTGAAGTCATCTCAGCTCTGCTCTATGATCACCTGCCACACTC 410		
:::: :::: :::: :::: ::::		
Db 1133 InHisValCysLeuHisAlaHisLahisLieuProLeuCystRpGlyAlaValCysProH 1153		
QY 409 ATCTTCCCTCTCTGAAATCAG 390		

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GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 20, 2003, 15:01:24 ; Search time 16.5 Seconds

(without alignments) 4205.500 Million cell updates/sec

Title: US-09-939-293-1

Perfect score: 2446

Sequence: 1 ggctccgcgcgtgcacaa.....ggacttaacacagaaaaaa 1358

Scoring table: BLOSUM62

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Ygapext 10.0 , Ygapext 0.5

Fgapext 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 280518

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPC=0 -DOOPENT=0 -UNITS=bis -SPART=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
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Database : Published_Applications_AA: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

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RESULT 1
US-09-925-297-591
; Sequence 591, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIORITY APPLICATION NUMBER: PCT/US00/05989
; PRIORITY FILING DATE: 2000-03-08
; PRIORITY APPLICATION NUMBER: 60124,270
; PRIORITY FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 591
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-297-591
Alignment Scores:
Pred. No.: 1.26e-92
Length: 227
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Score: 1138.00 ; LENGTH: 237
 Percent Similarity: 100.00% ; TYPE: PRT
 Best Local Similarity: 100.00% ; ORGANISM: Mus musculus
 Query Match: ; US-09-798-116-2
 DB: ;

QY 59 TCATTCCTCAGGTACAGACAGTGTGTTGGTCTGGTACTTAAGAGCGG 118
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 Db 2 SerphepheargtyArgglnlysleucyvalprovalalaisnphelysarg 21
 QY 119 TGTTCCTCAGGTGATAAGACCATGGCACAAACTGTGAGATTGCTTGAGTAACC 178
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 Db 22 CysPheSerGluLeuLeaProPheLysThrValThrIleGlyValThr 41
 QY 179 CTGTGCGCGGmVCTATGCCAGAACATCAGGCCATTCATCCCTAGTAGAACATGG 238
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 Db 42 LeucysAlaValProIleAlaGlnlysSerGluProIleSerGlnIleLeu 61
 QY 239 ATGAGGAGACAGTGCTTGGTACAGATAGCACCTCTACCTCTCTCTCAGACACA 298
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 Db 62 MetArgArgAlaValSerLeuValThrAspSerThrSerThrPheLeuSerGlnThrThr 81
 QY 299 TAGCGGTGTTGAACCTACTGATAACTAAGCTTATACTTAACCTACTCTCT 358
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 Db 82 TyraIleLeuIleGluAlaIleThrglytThrlysAlaValThrIleThrSerLeu 101
 QY 359 TACCGCAATATACAAAGTTACTTSGAAATAAGTAATGAACTTCAAGAGGAAGTG 418
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 Db 102 TyrAlaGlnIleThrSerLeuLeuGlyLysMetAspSerGluGluGluasp 121
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 Db 122 GlnValIleIleGlyIlaArgAlaGluMetThrSerIleGlyIleLeuIle 141
 QY 479 GAACCACTGTGATGACTGGAGTGGCTCTCAGAGATGGCAGAGAGTGCAATCAA 538
 ||||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 142 GlutHThrIlePheLeuAlaValGlyLeSerGluMetAlaAlaGluAlaAlaArg 161
 QY 539 ACTGGGCCAGATTCAGGCCTCTATAACGCCAGGAACTACAGTCAGTGAACTGAG 598
 ||||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 162 ThrGlyAlaAspGlnAlaSerIleLeuAlaAlaGlyIleGlnIle 181
 QY 599 GTGGAGAGGAGCACCAGCTCCCGGAAGCAGAACCAAGCTGGCAGACAGATA 658
 ||||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 182 ValGluGluValHisGlnLeuSerArgLysAlaGluIleGlyIleGlnIle 201
 QY 659 GAAGAGCTCCGTCAGAAACACAGGGAGAAGGGAGGGAGGAGGGCTGAGTG 718
 ||||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 202 GluGluLeuArgGlnLysIleGlnGluGluGlyIleGluGluArgAlaUserGluGlu 221
 QY 719 GCCTACTGCGCAGGAT 736
 Db 222 AlaryIleLeuArgGluasp 227

RESULT 2 ; Sequence 2, Application US/09798116
 ; Sequence 2, Application US/09798116
 ; Patent No. US20020110851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Verhagen, Anne Marie
 ; APPLICANT: Ekert, Paul
 ; APPLICANT: Vaux, David
 ; TITLE OF INVENTION: No. US20020110851A1 Polypeptides, Modulatory Agents Therefor an
 ; FILE REFERENCE: 10338-004US
 ; CURRENT FILING DATE: 2001-03-02
 ; PRIORITY APPLICATION NUMBER: AU PQ595/00
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patentin version 3.0

SEQ ID NO 2

US-09-798-116-2

QY 59 TCATTCCTCAGGTACAGACAGTGTGTTGGTCTGGTACTTAAGAGCGG 118
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2 SerphepheargtyArgglnlysleucyvalprovalalaisnphelysarg 21
 QY 119 TGTTCCTCAGGTGATAAGACCATGGCACAACTGTGAGATTGCTTGAGTAACC 178
 ||||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 22 CysPheSerGluLeuLeaProPheLysThrValThrIleGlyValThr 41
 QY 179 CTGTGCGCGGmVCTATGCCAGAACATCAGGCCATTCATCCCTAGTAGAACATGG 238
 ||||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 42 LeucysAlaValProIleAlaGlnlysSerGluProIleSerGlnIleLeu 61
 QY 239 ATGAGGAGACAGTGCTTGGTACAGATAGCACCTCTACCTCTCTCAGACACA 298
 ||||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 62 MetArgArgAlaValSerLeuValThrAspSerThrSerThrPheLeuSerGlnThrThr 81
 QY 299 TAGCGGTGTTGAACCTACTGATAACTAAGCTTATACTTAACCTACTCTCT 358
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 82 TyraIleLeuIleGluAlaIleThrglytThrlysAlaValThrIleThrSerLeu 101
 QY 359 TACCGCAATATACAAAGTTACTTSGAAATAAGTAATGAACTTCAAGAGGAAGTG 418
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 102 TyrAlaGlnIleThrSerLeuLeuGlyLysMetAspSerGluGluGluasp 121
 QY 419 CAGGTGATCATTAGGCCAGAGTGATGACTCTAACACCAAGAGTACTGTGAGTC 478
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 122 GlnValIleIleGlyIlaArgAlaGluMetThrSerIleGlyIleLeuIle 141
 QY 479 GAACCACTGTGATGACTGGAGTGGCTCTCAGAGATGGCAGAGAGTGCAATCAA 538
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 142 GlutHThrIlePheLeuAlaValGlyLeSerGluMetAlaAlaGluAlaAlaArg 161
 QY 539 ACTGGGCCAGATTCAGGCCTCTATAACGCCAGGAACTACAGTCAGTGAACTGAG 598
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 162 ThrGlyAlaAspGlnAlaSerIleLeuAlaAlaGlyIleGlnIle 181
 QY 599 GTGGAGAGGAGCACCAGCTCCCGGAAGCAGAACCAAGCTGGCAGACAGATA 658
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 182 ValGluGluValHisGlnLeuSerArgLysAlaGluIleGlyIleGlnIle 201
 QY 659 GAAGAGCTCCGTCAGAAACACAGGGAGAAGGGAGGGAGGGCTGAGTG 718
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 202 GluGluLeuArgGlnLysIleGlnGluGluGlyIleGluGluArgAlaUserGluGlu 221
 QY 719 GCCTACTGCGCAGGAT 736
 Db 222 AlaryIleLeuArgGluasp 227

RESULT 2 ; Sequence 2, Application US/09798116
 ; Sequence 2, Application US/09798116
 ; Patent No. US20020110851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Verhagen, Anne Marie
 ; APPLICANT: Ekert, Paul
 ; APPLICANT: Vaux, David
 ; TITLE OF INVENTION: No. US20020110851A1 Polypeptides, Modulatory Agents Therefor an
 ; FILE REFERENCE: 10338-004US
 ; CURRENT FILING DATE: 2001-03-02
 ; PRIORITY APPLICATION NUMBER: AU PQ595/00
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patentin version 3.0

SEQ ID NO 3

US-09-798-116-4

QY 20 ATGGCCGCTCTGAGAGTGTGCTGRCGCGAGCGTAACCTCATCTCAGGTACAGACAG 79
 ||||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 MetalAlaAlaLeuArgSerPheLeuValThrArgSerValCysSerLeuPheArgTyArgGln 20
 QY 80 TGTTTGTGTCGCTCTGCGCTACTTAAAGAAGGGGTTTCAGATGTGAGAAGA 139
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 21 ArgPhe-----ProValLeuIleLeuAspSerPheLeuValThrArgSerValCysSerLeuPheArgTyArgGln 38
 QY 140 CCATGCACAAACITGAGCATGCTTGGACTTAAAGCTTAACTTAACCTACTCTCT 199
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 39 ProTrpHisLysThrValLeuThrGlyPheIleMetThrGlyLysSerGlyPheSerGlnIleLeuIle 58
 QY 200 CAGAAATCAGGCCCTCATCCCTAGTAGTGAGGATGTGAGGAGGAGGTGCTTGTG 259
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 59 GlnLysSerGluProIleSerIleSerAspGlnIleLeuMetAspGlnAlaValSerIle 78
 QY 260 GTAAAGATGACCCCTACCTCTCTCAGACACATAGCGGTGATGAACTTATT 319
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 79 ValThrAspSerThrSerIleGlnIlePhelLeuSerGlnIleThrIleAlaLeuIleGluIle 98
 QY 320 ACTGAAATACTAAGCTGTTACTCTACTCTACTCTCTTACCGACATAACAGTTA 379
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 99 ThrglyIleThrlysAlaValThrIleLeuValSerIleLeuThrArgIleIleGlyIle 118
 QY 380 CTGGGAAATGATTAGCTAGAGGAGATAAGTGAGTGGAGGTGTCAGAGGCCAGA 439
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 119 LeuGlyLysMetAsnSerGlnIleGluGluAspGluValTrpGlnValIleIleGlyIle 138
 QY 440 GCTGAACTGACTCTAACACCAAGGTACTGTGAGGAACCATCTGGATGCTGCA 499
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 139 ValGluIleMetThrSerIleGlyIleGlyIleLeuIleGluIleThrIlePheLeuAla 158
 QY 500 GTGGCTCTCAGAGTGGCAGCAGAGCTCATCAACTGGCCAGATCAGCCCT 559
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 159 ValGlyIleUserGluMetAlaAlaGluAlaIleTyGlnIlePheGlyIleAlaAspGlnAlaSer 178
 QY 560 ATAACGCCAGGATCACATCAGCTGGTAACACTGAGGTCAGGAGGACCAAGCTC 619
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 179 IleThrAlaArgAsnIleGlnIleLeuVallysSerGlnValGlnGluValArgGlnLeu 198
 QY 620 TCCCGAAAGGAGAACCAAGCTGGAGAACAGCACAGAGACTCCCTCAGAAACA 679
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 199 SerGlnLysAlaIleGlyIleLeuIleAlaGluIleGlyIleHisGlnIleSala 218
 QY 680 CAGGAGGAGGGAGGAGCCGGCTGTGCGAGCAGGAGGCTACCTGGCTGAGGT 736
 ||||||| ||||| ||||| ||||| |||||
 Db 219 GlnGluValSerAspGlnIleGluGluIleIleGlyIleLeuIle 237

RESULT 3 ; Sequence 4, Application US/09798116
 ; Sequence 4, Application US/09798116
 ; Patent No. US20020110851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Verhagen, Anne Marie
 ; APPLICANT: Ekert, Paul
 ; APPLICANT: Vaux, David
 ; TITLE OF INVENTION: No. US20020110851A1 Polypeptides, Modulatory Agents Therefor an
 ; FILE REFERENCE: 10338-004US

CURRENT APPLICATION NUMBER: US/09/798,116 ; CURRENT APPLICATION NUMBER: US/09/798,116-7 ;
; PRIORITY APPLICATION NUMBER: AU PQ5995/00 ;
; PRIORITY FILING DATE: 2000-03-02 ;
; NUMBER OF SEQ ID NOS: 25 ;
; SOFTWARE: PatentIn version 3.0 ;
; SEQ ID NO: 4 ;
; LENGTH: 237 ;
; TYPE: PRT ;
; ORGANISM: Mus musculus ;
; US-09-798-116-4 ;
; Alignment Scores:
; Pred. No.: 7.57e-82
; Score: 1016.00
; Percent Similarity: 91.21%
; Best Local Similarity: 85.36%
; Query Match: 41.54%
; DB: 10
; Length: 237
; Matches: 204
; Conservative: 14
; Mismatches: 19
; Indels: 2
; Gaps: 1
; US-09-939-293-1 (1-1358) x US-09-798-116-4 (1-237)
; QY 20 ATGGCGGCTCTGAGAGTGGCTGTGCCAGCGTAACITCATTCAGGTACAGACAG 79
; Db 1 MetAlaAlaLeuLysSerGluSerGlyPheAspValThrArgSerValcys 20
; QY 80 TGTGTTGTTGTTCTGTTGGCTACTTAAAGAGCGGGTTTCAGATTGATAAGA 139
; Db 21 ArgPhe----ProValLeuAlaAsnSerLysLysArgSerGluLeuLys 38
; QY 140 CCTATGGCACAAACTGTGAGATGGCTTGTGAACTAACCCCTGTGGGTCTCTATGCA 199
; Db 39 ProTrpHisLysThrValLeuThrGlyPheGlyMetThrLeuCysAlaValProLeuAla 58
; QY 200 CAGAAATCGAGGCATCCCTAGTAGTGAGACATGTGAGGGAGGAGGTGCTTG 259
; Db 59 GluLysSerGluProHisSerLeuSerAsnGluAlaLeuMetTaGArgAlaSerLeu 78
; QY 260 GTTACAGAGATGACCTCTAACCTTCTCTAGACCCACATATGCCATTGAACTTATT 319
; Db 79 ValThrPheSerThrSerPheLeuSerGlnThrThyAlaLeuLysGluAlaIle 98
; QY 320 ACTGAAATACTAAAGCTGTATACCTAACTACTCTCTTACCGAACATACTAAGTTA 379
; Db 99 ThrGlyUryThrLysAlaValAltyrThrLeuValSerLeuValYrgLntyThrSerLeu 118
; QY 380 CTGGGAATGAAATCTCAGGGAGAGTAGAAGTGTGGAGGATCATAGGCCAGA 439
; Db 119 LeuGlyLysMetAsnSerGlnGluLysAspGluValTrpGlnValLeuIleGlyIlaArg 138
; QY 440 GCTGAGATGACTGAAACACCAAGAGTACTTGAGCTGGAAACCACTGATGACTGCA 499
; Db 139 ValGluMetThrSerLysGlnGlnGluLysLeuLysLeuGluThrThrPmEthAla 158
; QY 500 GTCGAGCTCTTCAGATGATGCGAGAAGGTGCAATCAACACTGGCGCAGTCAGCCTCT 559
; Db 159 ValGlyLeuSerGluMetAlaAlaGluAlaAlaTyrgInhThyAlaAspGlnAlaSer 178
; QY 560 ATACCGCCAGGAAATCACATCAGCTGGAAACTGCAGGGAGAGGGCACCAGCTC 619
; Db 179 IleThrAlaArgAsnHistLeuValLysSerGluValGluLysAlaArgInle 198
; QY 620 TCCGGAAAGCAGAACCAAGCTGGCAGAGCACAGATAGAGAGCTCCCTCAGAAACA 679
; Db 199 SerGlnLysAlaGluThrLysLeuAlaGluAlaGlnInhLysGluLeuHisGlnLysAla 218
; QY 680 CAGAGGAAGGGAGGAGCAGGGCTGAGTCGGAGGAGGAGGAGCCTACTGTGAGAT 736
; Db 219 GluGluValSerAspGluLysAlaAspGlnGluLysGluLysAlaValLeuArg 237
; RESULT 4
; Sequence 7, Application US/09798116

CURRENT APPLICATION NUMBER: US/09/798,116
 CURRENT FILING DATE: 2001-03-02
 PRIOR APPLICATION NUMBER: AU PQ5995/00
 PRIOR FILING DATE: 2000-03-02
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 9
 LENGTH: 84
 TYPE: PRT
 ORGANISM: Rattus sp.
 US-09-798-116-9

Alignment Scores:
 Pred. No.: 1.08e-21 Length: 84
 Score: 333.00 Matches: 68
 Percent Similarity: 86.05% Conservative: 6
 Best Local Similarity: 79.07% Mismatches: 10
 Query Match: 13.61% Indels: 2
 DB: 10 Gaps: 1

US-09-939-293-1 (1-1358) x US-09-798-116-9 (1-84)

QY 20 ATGGGGCTCTGAAAGAGTGTGGCTGCGCAGCGTAACTTCACTCTTCAGGTACAGACAG 79
 Db 1 MetAlaAlaLeuLargSerTriPmetThrArgSerValIthPhelLeuPheAlaGlyGlyGin 20

QY 80 TGTTRGTCGTTCTCGTGTGCTACTTGAAAGAGGCGGTRTCAGATGATAAGA 139
 Db 21 ArgPhe-----ProValSerAlaAsnSerLysArgCysPheSerGluLeuIarg 38

QY 140 CCATGCCACAACGCTGACGATGCTGGAGAACCTGTCGGTTCCATTGCA 199
 Db 39 ProTrpHisLysThrMetLeuThrGlyPheGlyLysAlaValProIleAla 58

QY 200 CAGAAATCAGAGCCATGCCATTGATCTAGTAGTAGTGAAAGCATGGAGGAGCAGTGCTTGTG 259
 Db 59 GlnLysSerGluProGlnSerLeuSerAsnGluAlaLeuMetArgGalaValSerLeu 78

QY 260 GAAZAGATAGCACCCT 277
 Db 79 ValThrAsnSerThrSer 84

RESULT 8

US-09-939-293-2

Sequence 2, Application US/09939293
 ; Patent No. US20020132786A1

GENERAL INFORMATION:

APPLICANT: Alnemri, Eman S.

TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
 FILE REFERENCE: 480140.465

CURRENT APPLICATION NUMBER: US/09/939,293

CURRENT FILING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 40
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-939-293-2

Alignment Scores:
 Pred. No.: 3.53e-09 Length: 40
 Score: 190.00 Matches: 40
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 7.77% Indels: 0
 DB: 10 Gaps: 0

US-09-939-293-1 (1-1358) x US-09-939-293-2 (1-40)

QY 185 GCGGTCTCTATGCAAGAAATCAGAGCCATCCCTAGTAGTGAAAGCATGATGAGG 244

RESULT 9

US-09-939-293-8

Sequence 8, Application US/09939293
 ; Patent No. US20020132786A1

GENERAL INFORMATION:

APPLICANT: Alnemri, Eman S.

TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
 FILE REFERENCE: 480140.465

CURRENT APPLICATION NUMBER: US/09/939,293

CURRENT FILING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 8
 LENGTH: 39
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-939-293-8

Alignment Scores:
 Pred. No.: 7.9e-09 Length: 39
 Score: 186.00 Matches: 39
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 7.60% Indels: 0
 DB: 10 Gaps: 0

US-09-939-293-1 (1-1358) x US-09-939-293-8 (1-39)

QY 185 GCGGTCTCTATGCAAGAAATCAGAGCCATCCCTAGTAGTGAAAGCATGATGAGG 244
 Db 1 AlaValProIleAlaGlnLysSerGluProIleThrSerLeuSerGluAlaLeuMetArg 20

QY 245 AGAGCAGTGCTTGTGCTACAGATGACCCCTCACCTCTCTCAGACACAT 301
 Db 21 ArgAlaValSerLeuValThrAspSerThrSerIlePheLeuSerGlnThrThrYrr 39

RESULT 10

US-09-939-293-11

Sequence 11, Application US/09939293
 ; Patent No. US20020132786A1

GENERAL INFORMATION:

APPLICANT: Alnemri, Eman S.

TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
 FILE REFERENCE: 480140.465

CURRENT APPLICATION NUMBER: US/09/939,293

CURRENT FILING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 11
 LENGTH: 35
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-939-293-11

Alignment Scores:
 Pred. No.: 6.67e-07 Length: 35
 Score: 164.00 Matches: 35
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.70% Indels: 0
 DB: 10 Gaps: 0

US-09-939-293-1 (1-1358) x US-09-939-293-11 (1-35)

QY 185 GCGGTCTCTATGCAAGAAATCAGAGCCATCCCTAGTAGTGAAAGCATGATGAGG 244

Db 1 AlavalproteAlaglnLysserGluProHisSerLeuSerGluAlaLeuMetArg 20
 Qy 245 AGGCAGTGCTTGGTAAACAGATGACCTTCACCTTCCT 289
 Db 21 ArgAlavalSerLeuValThrAppSerThrSerThrPheLeuSer 35
 RESULT 11
 ; Sequence 24, Application US/09798116
 ; Patent No. US20020110851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Verhaegen, Anne Marie
 ; APPLICANT: Ekert, Paul
 ; TITLE OF INVENTION: No. US20020110851A1 Polypeptides, Modularatory Agents Therefor an
 ; FILE REFERENCE: 10338-004US
 ; CURRENT APPLICATION NUMBER: US/09/798,116
 ; CURRENT FILING DATE: 2001-03-02
 ; PRIOR APPLICATION NUMBER: AU P05995/00
 ; PRIOR FILING DATE: 2000-03-02
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 24
 ; LENGTH: 32
 ; TYPE: PRT
 ; ORGANISM: synthetic
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (14)..(14)
 ; OTHER INFORMATION: M is methionine sulfoxide
 ; NAME/KEY: misc_feature
 ; LOCATION: (6)..(6)
 ; OTHER INFORMATION: M is methionine sulfoxide
 ; US:09-798-116-24
 Alignment Scores:
 Pred. No.: 2.68e-06 Length: 32
 Score: 157.00 Matches: 32
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.428 Indels: 0
 DB: 10 Gaps: 0
 US-09-798-116-10 (1-73)
 ; Sequence 24, Application US/09798116
 ; Patent No. US20020110851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Verhaegen, Anne Marie
 ; APPLICANT: Ekert, Paul
 ; TITLE OF INVENTION: AND METHODS OF USING THE SAME
 ; FILE REFERENCE: 480140.465
 ; CURRENT APPLICATION NUMBER: US/09/939,293
 ; CURRENT FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 7
 ; LENGTH: 30
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-939-293-7
 ; US-09-939-293-7
 Alignment Scores:
 Pred. No.: 6.78e-05 Length: 30
 Score: 141.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.768 Indels: 0
 DB: 10 Gaps: 0
 US-09-939-293-1 (1-1358) x US-09-798-116-10 (1-73)
 ; Sequence 10, Application US/09798116
 ; Patent No. US20020110851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Verhaegen, Anne Marie
 ; APPLICANT: Ekert, Paul
 ; APPLICANT: Vaux, David
 ; TITLE OF INVENTION: No. US20020110851A1 Polypeptides, Modularatory Agents Therefor an
 ; FILE REFERENCE: 10338-004US
 ; CURRENT APPLICATION NUMBER: US/09/798,116
 ; CURRENT FILING DATE: 2001-03-02
 ; PRIOR APPLICATION NUMBER: AU P05995/00
 ; PRIOR FILING DATE: 2000-03-02
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 10
 ; LENGTH: 73
 ; TYPE: PRT
 ; ORGANISM: Platichthys flesus
 ; US-09-798-116-10
 Alignment Scores:
 Pred. No.: 2.02e-05 Length: 73
 Score: 148.50 Matches: 30
 Percent Similarity: 81.97% Conservative: 20
 Best Local Similarity: 49.18% Mismatches: 8
 Query Match: 6.07% Indels: 3
 DB: 10 Gaps: 1
 US-09-939-293-1 (1-1358) x US-09-798-116-10 (1-73)
 ; Sequence 7, Application US/09939293
 ; Patent No. US20020132786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Almendri, Edad S.
 ; APPLICANT: Almendri, Edad S.
 ; TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
 ; TITLE OF INVENTION: AND METHODS OF USING THE SAME
 ; FILE REFERENCE: 480140.465
 ; CURRENT APPLICATION NUMBER: US/09/939,293
 ; CURRENT FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 7
 ; LENGTH: 30
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-939-293-7
 ; US-09-939-293-7
 Alignment Scores:
 Pred. No.: 6.78e-05 Length: 30
 Score: 141.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.768 Indels: 0
 DB: 10 Gaps: 0
 US-09-939-293-1 (1-1358) x US-09-939-293-7 (1-30)
 ; Sequence 25, Application US/09798116
 ; Patent No. US20020110851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Verhaegen, Anne Marie
 ; APPLICANT: Ekert, Paul
 ; APPLICANT: Vaux, David
 ; TITLE OF INVENTION: No. US20020110851A1 Polypeptides, Modularatory Agents Therefor an
 ; FILE REFERENCE: 10338-004US
 ; CURRENT APPLICATION NUMBER: US/09/798,116
 ; CURRENT FILING DATE: 2001-03-02
 ; PRIOR APPLICATION NUMBER: AU P05995/00
 ; PRIOR FILING DATE: 2000-03-02
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 10
 ; LENGTH: 73
 ; TYPE: PRT
 ; ORGANISM: Platichthys flesus
 ; US-09-798-116-25
 ; Sequence 25, Application US/09798116
 ; Patent No. US20020110851A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Verhaegen, Anne Marie
 ; APPLICANT: Ekert, Paul

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ON nucleic - protein search, using frame_plus_n2p model

Run on: February 20, 2003, 14:47:23 ; Search time 21.5 Seconds
(without alignments)
5239.521 Million cell updates/sec

Title: US-09-939-293-1

perfect score: 2446

Sequence: 1 ggcttcgcgcgtgcacaa.....ggacttaacacagaaaaaa 1358

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Xgapext	Ygapext	Score
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0.0	10.0	0.5
6.0	6.0	7.0
6.0	7.0	7.0

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Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=XGSPRO_spool/US099393/runat_20022003_111510_14829/app_query.fasta_1.1543
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdt -LIST=45
-DOCALIGN=200 -THR_SCORE_PCT -THR_MAX=100 -MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFILE="to_NORM-ext -HEAPSIZE=500 -MINLEN=100 -MAXLEN=2000000000
-USER-US099393_@CGN_1_1_30_@runat_20022003_111510_14829 -NCPU=6 -ICPU=3
-NO_XIPXY -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THRESHOLD=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1201	49.1	239	1 SMAC_HUMAN	Ognr28 homo sapien
2	1016	41.5	237	1 SMAC_MOUSE	09j193 mus musculus
C 3	125.5	5.2	502	1 WASP_HUMAN	P42768 homo sapien
C 4	112	4.6	3660	1 DMOC_CHICK	PI1533 gallus gallus
C 5	111	4.6	1323	1 NM24_MOUSE	003391 mus musculus
C 6	111	4.5	1323	1 NM24_RAT	062645 rattus norvegicus
C 7	110	4.5	589	1 SPY_DROME	044783 drosophila melanogaster
C 8	107.5	4.4	1520	1 TOP2_CABEL	023670 caenorhabditis elegans
C 9	106.5	4.4	3164	1 TECU_HSV1	P10220 herpes simplex virus type I
C 10	106	4.4	520	1 WASP_MOUSE	P70315 mus musculus
C 11	104.5	4.3	1219	1 JAG1_RAT	063722 rattus norvegicus
C 12	103.5	4.2	4684	1 PLE1_HUMAN	015149 homo sapien
C 13	103	4.2	592	1 LAN2_MOUSE	P21619 mus musculus
C 14	103	4.2	1433	1 REEN_CHICK	042184 gallus gallus
C 15	102.5	4.2	3924	1 ANK2_HUMAN	001484 homo sapien
C 16	102.5	4.2	5376	1 ZAN_MOUSE	088799 mus musculus
C 17	102	4.2	2116	1 MYS2_DCDC1	P08799 dictyostelia
C 18	101.5	4.2	500	1 FXE2_HUMAN	099526 homo sapien

RESULT 1

ID	SMAC_HUMAN	STANDARD;	PRT;	239 AA.
AC	O9NR28; Q9BP11; O9HAY6; Q36LV0;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Smac protein, mitochondrial precursor (Second mitochondria-derived activator of caspase) (Direct IAP binding protein with low pi).			
GN	SMAC OR DIABLO.			
OS	Homosapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Actinopterygii; Sarcopterygii; Gnathostomata; Tetrapoda; Amniota; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), PARTIAL SEQUENCE, FUNCTION, AND TISSUE SPECIFICITY			
RX	MEDLINE=20383536; PubMed=10929711;			
RA	Du C., Fang M., Li Y., Li L., Wang X.;			
RT	"Smac, a mitochondrial protein that promotes cytochrome c-dependent caspase activation by eliminating IAP inhibition.";			
RT	Cell 102:33-42(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T., Nakamura Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakagawa Y., Isogai T., Sugano S.; "NEKO human cDNA sequencing project"; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.			
RX	Pubmed=10930947;			
RA	Srinivasula S.M., Datta P., Fan X.J., Fernandes-Alnemri T., Huang Z., Alnemri E.S.;			
RT	"Molecular determinants of the caspase-promoting activity of Smac/DIABLO and its role in the death receptor pathway.";			
J. Biol. Chem. 275:36152-36157(2000).				
[4]	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Cerebellum;			
RA	Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,			

RX MEDLINE=20383537; PubMed=10929712;
 RA Verhagen A.M., Ebert P.G., Pakusch M., Silke J., Connolly L.M.,
 RA Reid G.E., Moritz R.L., Simpson R.J., Vaux D.L.;
 RT Identification of DIABLO, a mammalian protein that promotes apoptosis
 by binding to and antagonizing IAP proteins.";
 RL Cell 102:43-53(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RK MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shiba K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Noda J., Fukuda S.,
 RA Alzaga K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H., Ashburner M., Battalov S., Casavant T.,
 RA Fleischmann M.W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuura Y., Nikaido I., Pesce G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ringold M., Rodriguez I., Sakamoto N., Wagner L.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shiba K., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C.,
 RA Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H.,
 RA Kohtsuji S.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001)
 CC 1- FUNCTION: PROMOTES APOPTOSIS BY ACTIVATING CASPASES IN THE
 CYTOCHROME C/APAF-1/CASPASE-9 PATHWAY. ACTS BY OPPOSING THE
 INHIBITORY ACTIVITY OF AN INHIBITOR OF APOPTOSIS PROTEINS (IAP).
 CC -1- SUBUNIT: Homodimer. Interacts with BIRC2, BIRC3, BIRC4/XIAP and
 BIRC7 (BY similarity).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL BUT RELEASED INTO THE CYTOSOL
 WHEN CELLS UNDERGO APOPTOSIS.
 CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION FOUND IN HEART, LIVER,
 CC KIDNEY AND TESTIS.
 CC -1- DOMAIN: The mature N-terminus mediates interaction with
 BIRC4/XIAP (BY similarity).
 CC
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 CC
 DR EMBL; AF203914; AAF82190; 1;
 DR EMBL; AK012760; BAB24450; 1;
 DR EMBL; AK02887; BAB24433; 1; ALT FRAME.
 DR HSSP; Q9NRZ8; IFEW.
 DR MGD: MGI:1913843; 0610041G12Rik.
 KW TRANSIT peptide; Mitochondria; Apoptosis.
 FT CHAIN 53 MITOCHONDRIUM (BY SIMILARITY).
 FT SITE 54 237 SMAC PROTEIN.
 FT CONFLICT 58 IAP-BINDING MOTIF (BY SIMILARITY).
 SQ SEQUENCE 237 AA; 26829 MW; E53EBP04FC390A1 CRC64;

RESULT 3

WASP_HUMAN	ID	WASP_HUMAN	STANDARD	PRT	502 AA.
AC	P42768; Q9UNQ9; Q9BUU1;	DT	01-OCT-1995 (Rel. 32, created)		
DT	01-OCT-1996 (Rel. 34, last sequence update)	DT	15-JUN-2002 (Rel. 41, last annotation update)		
DE	Wiskott-Aldrich syndrome protein (WASP).	GN	WAS OR IMD2.		
OS	Homo sapiens (Human).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OX	NCBI_TaxID:9606;		
RN	[1]	RP	SEQUENCE FROM N.A.		
RC	TISSUE-T-cell;	RX	MEDLINE=94349367; PubMed=8069912;		
RA	Derry J.M.J., Ochs H.D., Francke U.;	RT	"Isolation of a novel gene mutated in Wiskott-Aldrich syndrome.";		
RL	Cell 78:635-644(1994).	RN	Cell 79:923-923(1994).		
RP	ERRATUM.	RX	MEDLINE=95094263; PubMed=8001129;		
RA	Derry J.M.J., Ochs H.D., Francke U.;	RL	Cell 79:923-923(1994).		
RN	[3]				

US-09-939-293-1 (1-1358) x SMAC_MOUSE (1-237) 79

- RP SEQUENCE FROM N.A.
 RX MEDLINE=9527432; PubMed=7753869;
 RA Kwan S.P., Hagemann T.L., Radtke B.E., Blaese R.M., Rosen F.S.;
 RT "Identification of mutations in the Wiskott-Aldrich syndrome gene and characterization of a polymorphic dinucleotide repeat at DXS6940, adjacent to the disease gene.";
 RT proc. Natl. Acad. Sci. U.S.A. 92:4706-4710(1995).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9167346; PubMed=10066431;
 RA Hagemann T.L., Kwan S.-P.;
 RA "The identification and characterization of two promoters and the complete genomic sequence for the Wiskott-Aldrich syndrome gene.";
 RL Biochem. Biophys. Res. Commun. 256:104-109(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Nyakatura G., Strom T.M., Drescher B., Menzel U., Meindl A., Rosenthal A.;
 RA submitted (OCT-1999) to the EMBL/GenBank/DDJB databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Straubberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDJB databases.
 RN [7]
 RP VARIANTS WAS K-31; M-75; P-82; C-86; H-86; C-97; K-133; E-476 AND H-30 DEL.
 RX MEDLINE=96133285; PubMed=8528198;
 RA Kolluri R., Shehabeldin A., Peacock M., Lamhonwah A.-M., Teichert-Kuliszewska K., Weissman S.M., Siminovitch K.A.;
 RT "Identification of WASP mutations in patients with Wiskott-Aldrich syndrome and isolated thrombocytopenia reveals allelic heterogeneity at the WAS locus.";
 RL Hum. Mol. Genet. 4:1119-1126(1995).
 RN [8]
 RP VARIANTS WAS F-27; I-48; M-75; L-86; H-86; K-131; C-187 AND K-477.
 RX MEDLINE=96133286; PubMed=8528199;
 RA Derry J.M.J., Kerns J.A., Weinberg K.I., Ochs H.D., Volpini V., Estivill X., Walker A.P., Francke U.;
 RT "WASP gene mutations in Wiskott-Aldrich syndrome and X-linked thrombocytophenia.";
 RL Hum. Mol. Genet. 4:1127-1135(1995).
 RN [9]
 RP VARIANTS WAS VAL-56 AND GLU-236.
 RX MEDLINE=9531593; PubMed=779548;
 RA Villa A., Notarangelo L., Mantuano E., Cavagni G., Brugnoni D., Surina D., Patrosso M.C., Ramenghi U., Sacco M.G., Ugazio A., Vezzoni P.;
 RT "X-linked thrombocytopenia and Wiskott-Aldrich syndrome are allelic diseases with mutations in the WASP gene.";
 RL Nat. Genet. 9:414-417(1995).
 RN [10]
 RP VARIANTS WAS TRP-43; MET-45; MET-75 AND CYS-86.
 RX MEDLINE=9722113; PubMed=9126958;
 RA Remold-O'Donnell E., Cooley J., Sicherman A., Hagemann T.L., Kwan S.-P., Kenney D.M., Rosen F.S.;
 RT "Variable expression of WASP in B cell lines of Wiskott-Aldrich syndrome patients.";
 RL J. Immunol. 158:4021-4025(1997).
 RN [11]
 RP VARIANTS WAS LYS-31 AND MET-45.
 RX MEDLINE=9725413; PubMed=9098856;
 RA Ariga T., Yamada M., Sakiyama Y.;
 RT "Mutation analysis of five Japanese families with Wiskott-Aldrich syndrome and determination of the family members' carrier status using three different methods.";
 RL Pediatr. Res. 41:535-540(1997).
 RN [12]
 RP VARIANTS WAS MET-75; LEU-84; ASP-89 AND LYS-133.
 RX MEDLINE=9835091; PubMed=9683546;
 RA MacCarthy-Morrogh L., Gaspar H.B., Wang Y.-C., Katz F., Thompson L., Layton M., Jones A.M., Kinnon C.;
 RA "Absence of expression of the Wiskott-Aldrich syndrome protein in peripheral blood cells of Wiskott-Aldrich syndrome patients.";
 RL Clin. Immunol. Immunopathol. 88:22-27(1998).
 RA Kwan S.P., Hagemann T.L., Radtke B.E., Blaese R.M., Rosen F.S.;
 RT VARIANT WAS VAL-56.
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98378988; PubMed=9713366;
 RA Facchetti F., Blanzoli L., Vermi W., Notarangelo L.D., Giliani S., Fiorini M., Pastan A., Stewart D.M., Nelson D.L.;
 RT "Defective actin polymerization in EBV-transformed B-cell lines from patients with the Wiskott-Aldrich syndrome.";
 RL J. Pathol. 185:99-107(1998).
 RN [14]
 RP VARIANTS WAS LYS-133.
 RX MEDLINE=98092074; PubMed=9445409;
 RA Parolini O., Reissmann G., Haas O.A., Pawlowsky J., Gardner H., Knapp W., Holter W.;
 RT "X-linked Wiskott-Aldrich syndrome in a girl.";
 RL New Engl. J. Med. 338:291-295(1998).
 RN [15]
 RP VARIANTS WAS ARG-73; MET-75; CYS-83; CYS-86 AND LYS-133.
 RX MEDLINE=98374925; PubMed=10447259;
 RA Lemarie V., Gastier J.M., Francke U.;
 RT "Novel mutations in the Wiskott-Aldrich syndrome protein gene and their effects on transcriptional, translational, and clinical phenotypes.";
 RT Hum. Mutat. 14:54-66(1999).
 RL [16]
 RP VARIANTS WAS HIS-52 AND TRP-70.
 RX MEDLINE=21652748; PubMed=11793485;
 RA El-Hakem J., Rosemurgy S., Oleastro M., Bassack N., Berozdnik L., Molina F., Rivas E.M., Zelazko M., Danielian S.;
 RT "Wiskott-Aldrich syndrome in Argentina: 17 unique, including nine novel, mutations.";
 RL Hum. Mutat. 19:186-187(2002).
 CC -!- FUNCTION: POSSIBLE REGULATOR OF LYMPHOCYTE AND PLATELET FUNCTION. MAY BE INVOLVED IN SIGNALING PATHWAYS WITH CYTOSKELETAL FUNCTION.
 CC -!- SUBUNIT: BINDS TO CIC42, RAC, NCK, FYN, SRC KINASE FGR, BTK, ABL, WIP, AND TO THE P85 SUBUNIT OF PLC-GAMMA.
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE THYMUS. ALSO FOUND TO A MUCH LESSER EXTENT, IN THE SPLEEN.
 CC -!- DOMAIN: THE WH1 (WASP HOMOLOGY 1) DOMAIN MAY BIND A PRO-RICH LIGAND.
 CC -!- DISEASE: DEFECTS IN WASP ARE THE CAUSE OF WISKOTT-ALDRICH SYNDROME (WAS), AN X-LINKED RECESSIVE IMMUNODEFICIENCY CHARACTERIZED BY ECZEMA, THROMBOCYTOPENIA, RECURRENT INFECTIONS, AND BLOODY DIARRHEA. DEATH USUALLY OCCURS BEFORE AGE 10.
 CC -!- DISEASE: DEFECTS IN WASP ARE THE CAUSE OF ISOLATED X-LINKED THROMBOCYTOPENIA (XLT). XLT IS CLINICALLY MILD WITH SMALL PLATELETS AND SUBCLINICAL LEUKOCYTE ABNORMALITIES.
 CC -!- SIMILARITY: CONTAINS 1 CRIB DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 WH1 DOMAIN.
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- CC DR EMBL: U12707; AAA62663_1; ALT_SEQ.
 DR EMBL: U18935; AAA60381_1; --.
 DR EMBL: UI9927; AAC50140_1; --.
 DR EMBL: AF115543; AAC026691_1; --.
 DR EMBL: AF196970; AAC06804_1; --.
 DR EMBL: BC012961; AAC02961_1; ALT_INIT.
 DR EMBL: BC012738; AAC12738_1; --.
 DR Genew: HGNC:12731; WAS.
 DR MIM: 300392; --.
 DR MIM: 301000; --.
 DR InterPro: IPRO00095; PAKbox/Rhobnind.
 DR InterPro: IPRO00697; RanBP1_WASP.
 DR InterPro: IPRO01960; WH2.
 DR InterPro: IPRO03124; WH2.

CC	SENSITIVITY TO MAGNESIUM, MEDIATED BY GLYCINE.	Alignment Scores:	1.27
CC	- - SUBUNIT: HETERO-DIMER OF AN EPSONIC SUBUNIT AND A ZETA SUBUNIT.	Pred. No.:	11.00
CC	- - SUBCELLULAR LOCATION: Integral membrane protein.	Score:	56
CC	- - ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 AND 2 (SHOWN HERE); MAY BE	Percent Similarity:	31.37%
CC	BRODUCED BY ALTERNATIVE SPlicing.	Best Local Similarity:	27.45%
CC	- - TISSUE SPECIFICITY: EXPRESSED IN BRAIN, MAINLY IN THE SUBCORICAL REGION.	Query Match:	4.60%
CC	- - DEVELOPMENTAL STAGE: Already detected in embryonic stages, peaks at postnatal day 7, and decreases thereafter to adult levels.	DB:	Gaps:
CC	- - SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.	OY	915 GCAAGCTGAGACCAAGAGGGCACTCACAGCTCAAAGCGTCTCGCTGATGGCCA 856
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CC	CC	OY	855 GGGCAGCAGCCCTGCCTCTGTCGAGACAGTCAGGCCAACCCCTGGCAGGGTG 796
CC	CC	OY	765 -----GGACAGGGCAGTGTGTCAGGCCCTAACCTCACCGAGTAGCC 718
CC	CC	OY	1064 GlnProLeuIleGlyGlyGlyIala-----GlyGlyProSerAlaGly-AlaProThrI 1081
CC	DR	OY	717 TCCTGCCTCCGACTCACCCGCTCCCTCC-----CTTCCTCCCTGTGTT 676
DR	EMBL: D13214; BAA02501.1;	OY	1044 AlaPheGluAspGluSerProProAlaProSerArgTrpProArgSerAspProGluSer 1063
DR	EMBL: L31611; AAC37646.1;	OY	1081 aProProProArgArgGalaAlaProProProCysAlaTyLeuAspLeuGluPro 1101
DR	EMBL: L31612; AAC37647.1;	OY	675 TTCTGAG-----GGACGCTCTATGCTGCTGCTGAGCAGTCGTGACCT----- 606
DR	EMBL: U08260; AAC1833.1;	OY	1101 oSerAspSerGluAspSerGluSerIleGlyGlyIalaSerIleGlyGlyIleGluProTr 1121
DR	HSSP: P11491; IGR2.	OY	1121 pTrpPheAlaAspPheProTyroProTyraAlaGluArgLeuGlyProProProGlyArgTy 1141
DR	InterPro: IPR01130; Ion_glu_receptor.	OY	605 -----CTTCAGCTGC 595
DR	InterPro: IPR01311; SBP_glu_receptor.	OY	1141 rTrpSerValAspLysIleGlyGlyIleGlyIleGlyIleGluProTr 1161
KW	Pfam: PF00060; lig Chan.	OY	594 AGTTCAACCT-----GAATGATGCTGGGGTAGAGCCGATCT 547
KW	PRINTS: PRO0177; NMDA RECEPTOR.	OY	1161 gGlyGlyProIleAlaPheIleGlyIleGlyIleLeuIleProProProAr 1181
FT	prodrom: PP00050; Ion_glu_receptor; 1.	OY	546 GCGCCAGTTGATAAGCAGCTCTGCTGCAAGACCACTGAGTCATCAA 487
FT	Receptor; Signal; Transmembrane; Postsynaptic membrane; Calcium; Glycoprotein; Ionic channel; Magnesium; Alternative splicing.	OY	1181 gHis-----LeuSerCysSerHisAspGlyLeuAspGlyGlyTr 1194
FT	SIGNAL	OY	486 GTGGTTCCA 477
FT	CHAIN	OY	1194 pTrpAlaPro 1197
FT	28	RESULT 7	SPY_DROME
FT	1323	ID	SPY_DROME_STANDARD;
FT	1323	PRT	589 AA.
FT	1323	DT	16-OCT-2001 (Rel. 40, Last sequence update)
FT	1323	DT	16-OCT-2001 (Rel. 40, Last annotation update)
FT	1323	DT	16-OCT-2001 (Rel. 40, Last annotation update)
FT	1323	GN	Die protein sprouty (spry).
FT	1323	OS	STY OR CG19121.
FT	1323	OC	Drosophila melanogaster (Fruit fly).
FT	1323	OC	Eukaryota; Metazoa; Pancrustacea; Hexapoda;
FT	1323	OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
FT	1323	OC	Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.
FT	1323	OC	Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.
FT	1323	NCBI_TaxID	7227;
FT	1323	RN	[1]
FT	1323	RP	SEQUENCE FROM N-A.
FT	1323	RC	SPRAYIN=Cantron-S;
SEQUENCE	1323 AA; 143100 MW; 40FFD60192519564 CRC64;	RX	MEDLINE=98117253; PubMed=9458049;

RT	"Sprouty encodes a novel antagonist of FGF signaling that patterns apical branching of the <i>Drosophila</i> airways.";
RL	Cell 92:253-263(1998).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Berkeley;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gail R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H.C., Blazquez R.G., Champe M., Preiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agayamian A., An H.-J., Andrews P., Pfannkoch C., Baldwin D., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolstakov S., Borukova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Cherry J.M., Cowley S., Dahake C., Davenport L.B., Davies P., de Pablo B., Belcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doupe L.E., Downes M., Dugan-Rocha S., Dunkin P., Durbin R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Geibart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jaiswal B., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levittsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M., McPherson D., Merklikov G., Milshina N.V., Mobarry C., Morris J., Moskrafi A., Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamas T., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.-H., Wang X., Wang Z.-Y., Wasaman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L., Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of <i>Drosophila melanogaster</i> ."; Science 287:2185-2195(2000). [3]
RT	FUNCTION.
RX	MEDLINE=99387981; PubMed=10457022;
RA	Reich A., Sapir A., Shilo B.-Z.;
RT	"Sprouty is a general inhibitor of receptor tyrosine kinase signaling.";
RL	Development 126:4139-4147(1999).
RN	[4]
RP	FUNCTION.
RX	MEDLINE=99244704; PubMed=10226010;
RA	Kramer S., Okabe M., Racchoen N., Krasnow M.A., Hirano Y., "Sprouty: a common antagonist of FGF and EGF signaling pathways in <i>Drosophila</i> ,"; Development 126:2515-2525(1999).
CC	[5]
RP	FUNCTION, AND SUBCELLULAR LOCATION.
RX	MEDLINE=9918971; PubMed=10089881;
RA	Cascal T., Vinos J., Freeman M.; "Sprouty, an intracellular inhibitor of Ras signaling.";
RT	Cell 96:655-665(1999);
RL	Development 126:2515-2525(1999).
RN	-
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RN	-
RP	FUNCTION, AND SUBCELLULAR LOCATION.
RX	MEDLINE=9918971;

DR PIR: I30085; WMBEH6
DR InterPro: IPR005210; Herpes_Ul36.
DR Pfam: PF03586; Herpes_UL36; 1.
DR Repeat.
DR DOMAIN: 2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q.
DR SEQUENCE: 3164 AA; 335857 MW; CC5D31F4F9FB3F4 CRC64;
DR
DR Alignment Scores:
DR Pred. No.: 3.04 Length: 3164
DR Score: 106.50 Matches: 85
DR Percent Similarity: 33.12% Conservative: 21
DR Best Local Similarity: 26.56% Mismatches: 129
DR Query Match: 4.41% Indels: 85
DR DB: 1 17 Gaps: 17
DR
DR US-09-939-293-1 (1-1358) x TEGU_HSV1 (1-3164)
DR
DR QY 1252 CAGCTGTCCTCACAGACAGCAGGGCAGATCA-----GAG 1217
DR DB 2581 GluLeuAlaSerAspAspSerPrglyPrglyProLapProLeuLeuAlaProAspBProLeuUser 2600
DR QY 1216 AACACATGAAATCACATAAAGAAATCGTACACTGGACAGGTTCCCTTCG 1157
DR DB 2601 ProThrAlaAspGlnUserValProThrSerIncySlaProArg-ProProGlyProAl 2620
DR QY 1156 CACAAC-----GGCATCCAAAGAGGAAACAGGGCGC 844
DR DB 2620 AvaThrAlaArgGluAlaArgPrglyValProAlaGluSerThrArgProAla---- 2638
DR QY 1114 TTGAGCAGCTTAATAGACAGAACAGGTAAACAGTGTCTGAACCTAAGGCATG 1055
DR DB 2639 -----ProValGlyProArgAspAspPheAr 2647
DR QY 1054 AAAA---AGGACTCTCTCTGACCCAGGTAGGCCAAATGCTTGGTGAGGTAAA 998
DR DB 2647 9ArgLeuProSerProInSerSerProAlaProProAspLathAlaProArgProPr 2667.
DR QY 997 AAAATGGTAGGAGGAGCTGTACAGTGAGGTAAACAGGGTCAGGCCA 938
DR DB 2667 OAlaserSerArgAla-----SerAlaAlaserSerSe 2678
DR QY 937 AGGGTAAGAACCCAGTCCAGCGCAAGCTCAGACACAGGGGACTCACGTCACAA 878
DR DB 2678 rGlySerArgAlaArgGargHisArgAlaArgSerLeuAlaArgAlaThrGlnAlaSer 2698
DR QY 877 AGGCCTCTCCCTGATGGCCAGGCAGGCCTGCGCCTCTCTGGTGCACAGCAGT 818
DR DB 2698 rAlaThrThrGlnGlyTrp-----ArgProProAlaLeu--ProAspHrv 2713
DR QY 817 CATGCCAACCTGGCGAGGGTG--GCATCTGCCCTGCTTCCCCACTGAGTGGGAGA 761
DR DB 2713 1AlaProValThrAspPheAlaArgProProAlaProProLysProProGluProAlaPr 2733
DR QY 760 CAGGCCAGTGCTCAGGCCCTC-----AATCCTCACCCAGGTAGGCCCTG 713
DR DB 2733 OHisAlaLeuValSerGlyValProLeuProLeuGlyProGlnAlaAlaGlyGlnAlas 2753
DR QY 712 CTCCCACTCAGCCCTCCRCCTCTGCTGSPHTTCGACGAGCCTTCATCTG 653
DR DB 2753 erProAlaLeuProLeuAspProAlaProProProAlaIaThrGly-----T 2769
DR QY 652 TGCCTCTGCCAGCTCTGTT-----CTGCCCTCCGGAGAGCTGTCGCC 608
DR DB 2769 hrvAlaLeuProGlyGlyGluasnFargProProLeuThrSerGly-----ProAlaPr 2787
DR QY 607 CTCTCCACCTGAGGTTCACCGCTGAATGTGATMCTGCGGGTTATAGGCGCAGTC 548
DR DB 2787 roThProProArgVal--ProValGlyGlyProGlnArgGluLeuThrArgPro---- 2804
DR QY 547 TGCCGAGTTGATATGCAGCTCTGCTGAAAGACCAACTGAGCTA---- 492
DR CC or send an email to license@isb-sib.ch).
DR EMBL: X14112; CAA32311; -

QY 491 --TCCAGGGTTCCAGCTCAACTCTGTTGTTTG----- 453
 Db 2817 rothrSerSer----- SerProAlaGlyProSerProPro 2837

QY 452 --AAGTCATOTCAGCTGGCTCTATGACCTGCCAACATTCATCTCTCT 399
 Db 2837 rothrSerSer----- SerProAlaGlyProSerProPro 2849

RESULT 10
 WASP_MOUSE STANDARD; PRT; 520 AA.

ID WASP_MOUSE STANDARD; PRT; 520 AA.
 AC P70315;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Wiskott-Aldrich syndrome protein homolog (WASP).
 GN WASP OR WASP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10909;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=95115600; PubMed=8666397;
 RA Derry J.M.J., Wiedemann P., Blair P., Wang Y., Kerns J.A., Lemarie V., Godfraind V.L., Wilkinson J.E., Francke U.;
 RT "The mouse homolog of the Wiskott-Aldrich syndrome protein (WASP) gene is highly conserved and maps near the scurfy (sf) mutation on the X chromosome.";
 RT Genomics 29:471-477(1995).
 RL MAY BE INVOLVED IN SIGNALING PATHWAYS WITH CYTOSKELETAL FUNCTION.
 CC (BY SIMILARITY).
 -!- DOMAIN: THE WH1 (WASP HOMOLOGY 1) DOMAIN MAY BIND A PRO-RICH LIGAND.
 CC !- SIMILARITY: CONTAINS 1 CTRB DOMAIN.
 CC !- SIMILARITY: CONTAINS 1 WH1 DOMAIN.
 CC
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RESULT 11
 ID JAG1_RAT STANDARD; PRT; 1219 AA.
 AC Q63722; P70640;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Jagged 1 precursor (Jagged1).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Sciatic nerve;
 RX MEDLINE=95211842; PubMed=7697721;
 RA Lindseil C.E., Shawber C.J., Boulier J., Weinmaster G.;
 DR InterPro; IPR000697; Ranbp1_WASP.
 DR InterPro; IPR001960; WH1.
 DR InterPro; IPR003124; WH2.
 DR Pfam; PF00568; WH1; 1.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF0225; WH2; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00461; WH1; 1.
 DR SMART; SM0246; WH2; 1.
 DR PROSITE; PS50108; CRIB; 1.
 KW Repeat.
 FT DOMAIN 41 147 WH1.
 FT DOMAIN 240 253 CRIB.
 FT REPEAT 354 363 GRSGPLPPXP MOTIF 1.
 FT REPEAT 393 402 GRSGPLPPXP MOTIF 2.
 FT DOMAIN 162 167 POLY-PRO.
 FT DOMAIN 314 321 POLY-PRO.
 FT DOMAIN 324 341 POLY-GLY.
 FT DOMAIN 368 373 POLY-PRO.
 FT DOMAIN 376 379 POLY-PRO.
 FT DOMAIN 384 390 POLY-PRO.
 FT DOMAIN 397 403 POLY-PRO.
 FT DOMAIN 408 424 POLY-PRO.

FT DOMAIN 503 520 ASP/LEU-RICH (ACIDIC).
 SQ SEQUENCE 520 AA; 54191 MW; 9c22373c59f0c8a CRC64;

Alignment Scores:
 Pred. No.: 2.6 Length: 520
 Score: 106.00 Conservat.ve: 37
 Percent Similarity: 44.4% Matches: 3
 Best Local Similarity: 41.1% Mismatches: 33
 Query Match: 4.398 Index: 17
 DB: Gaps: 2

US-09-939-293-1 (1-1358) x WASP_MOUSE (1-520)

QY 808 CCTGGGCAGGGGATCTGCCCTGTCTTCCCACTGAGTGGGAGAGGGAGTGTG 749
 Db 379 PROGYIArgIArgIArgIArgIArgIArgIArgIArgIArgIArgIArgIArgIPro 398

QY 748 CTAGGCCCTCAACTCTCCGGCAGTAGGCCCTGCTCGACTCAGGCCGCTCTCCC 689
 Db 399 ProProProLeu-ProProIAlaGlyIProProProProProProProProPro 418

QY 688 TTCCCTCTGTTCTGAGGAGCTCTATCTGTTCTGCCAGCTGGTTCTG 629
 Db 445 ProGlyIArgIArgIArgIAlaLeu 452

Db 418 ProProProProProCysProPro----- 425

QY 628 TTCCGGGAGAGCTGTGACCTTCCACCTGCA--GTTTACCAAGCTGAATGTGATT 572
 Db 426 --Sergly-ProIAlaProProProLeuProProProIAlaProProProPro 444

QY 571 CCTSGCGGTATAAGGCCCTGATC 548

Db 445 ProGlyIArgIArgIArgIAlaLeu 452

RESULT 11
 ID JAG1_RAT STANDARD; PRT; 1219 AA.
 AC Q63722; P70640;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Jagged 1 precursor (Jagged1).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Sciatic nerve;
 RX MEDLINE=95211842; PubMed=7697721;
 RA Lindseil C.E., Shawber C.J., Boulier J., Weinmaster G.;
 DR InterPro; IPR000697; Ranbp1_WASP.
 DR InterPro; IPR001960; WH1.
 DR InterPro; IPR003124; WH2.
 DR Pfam; PF00568; WH1; 1.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF0225; WH2; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00461; WH1; 1.
 DR SMART; SM0246; WH2; 1.
 DR PROSITE; PS50108; CRIB; 1.
 KW Repeat.
 FT DOMAIN 41 147 WH1.
 FT DOMAIN 240 253 CRIB.
 FT REPEAT 354 363 GRSGPLPPXP MOTIF 1.
 FT REPEAT 393 402 GRSGPLPPXP MOTIF 2.
 FT DOMAIN 162 167 POLY-PRO.
 FT DOMAIN 314 321 POLY-PRO.
 FT DOMAIN 324 341 POLY-GLY.
 FT DOMAIN 368 373 POLY-PRO.
 FT DOMAIN 376 379 POLY-PRO.
 FT DOMAIN 384 390 POLY-PRO.
 FT DOMAIN 397 403 POLY-PRO.
 FT DOMAIN 408 424 POLY-PRO.

CC !- SIMILARITY: CONTAINS 1 DSL DOMAIN.

CC
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Db 815 ProaspCysArgIleAsnIleAsnGluCysGlnSerSerProCys--AlapheGlyala 833
 Qy 970 ACTCGT-----"TACAGCTGCCTAACCAATTACCTCACACC 1011
 Db 834 ThrcysValAspGluIleAsnGlyYrgCysIleCyspro... 847
 Qy 1012 CAAGCATTGCCAACCTGGTCAGAGAGAGTCCTTTGTCATGCCCTAAAGTC 1071
 Db 848 -----"ProGlyHisSerGlyIallyLysCysHisGluValSerGly 860
 Qy 1072 AGCAACTGTAACTCGTGTTCAGCTCTAACAAATGATTTAGRACTGT 1131
 Db 861 ArgSerCysIleThrMetGlyArgValleLeuAspGlyAlaLysTrpaspaspCys 880
 Qy 1132 TCCCTGT-----"TGGATGCCAGTGT 1155
 Db 881 AsnThrCysIleCysLeuAsnGlyArgValAlaCysSerLysValTrp-----Cys 897
 Qy 1156 GGC-----"AGGGGAGGGAACTGTCGA 1179
 Db 898 GlyProArgProCysArgIleHisLysGlyHsGlyLysProAsnGlyInSerCys 917
 Qy 1180 GTTGCTACGATTCTGTATGATTTCTGATGATGTTCTGCTGACTGCCCTACGT-- 1236
 Db 918 IleProValleAspAspGlnCysPheValArgProCysThrGlyIalaGlyLysCysArg 937
 Qy 1237 --"CCGTGAGAACGCTGAGCCAAGGAGTGAAAACCTTAATGAC 1281
 Db. 938 SerSerSerIeugInProValleThrPheAsnLysGluMetMetSerProGly 954
 Qy 1282 TAAGAAAGGGGCCAGACTGTCTCACAGGACTAACATCACAGGA 1341
 Db 955 --"GlnAspAsnCysAlaAsnIleThrPheThrPheAsnLysGluMetMetSerProGly 973
 Qy 1342 CTTAACACAGAA 1353
 Db 974 LeuThrThrGlu 977

RESULT 12

PLEL_HUMAN STANDARD; PRT: 4684 AA.

ID PLEL_HUMAN STANDARD; PRT: 4684 AA.
 AC Q15149; Q16640; Q15148;
 DT 16-OCT-2001 (Rel. 40, created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Plectin 1 (PLRN) (Hemidesmosomal protein 1) (HDL).
 GN PLEC1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1] NCBI_TaxID=9606;

RC SEQUENCE FROM N. A. (ISOFORM 1).

RC TISSUE=Placenta;
 MEDLINE=96210032; PubMed=8633055;
 RA Liu C.-G., Maercker C., Castanon M.J., Hauptmann R., Wiche G.;
 RT "Human plectin: organization of the gene, sequence analysis, and
 chromosome localization (8924)." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
 RN [2] SEQUENCE FROM N. A. (ISOFORMS 2 AND 3), AND DISEASE.
 MEDLINE=96312447; PubMed=8658233;
 RA McLean W.H.I., Punkkinen L., Smith F.J.D., Rugg E.L., Lane E.B.,
 RA Bullrich F., Burgess R.E., Amano S., Hudson D.L., Owaribe K.,
 RA McGrath J.A., McMillan J.R., Eady R.A.J., Leigh I.M., Christiano A.M.,
 RA Utto J.;
 RT "Loss of plectin causes epidermolysis bullosa with muscular dystrophy:
 cDNA cloning and genomic organization." ;
 Genes Dev. 10:1724-1735(1996).
 RN [3] VARIANT MD-EBS 1003-GLN-ALA-1005 DEL.
 MEDLINE=97049959; PubMed=8894687;

RN 815 ProaspCysArgIleAsnIleAsnGluCysGlnSerSerProCys--AlapheGlyala 833
 RA Pulkkinen L., Smith F.J.D., Shimizu H., Murata S., Yaoita H.,
 RA Hachisuka H., Nishikawa T., McLean W.H.I., Utto J.;
 RT "Homozygous deletion mutations in the plectin gene (PLEC1) in patients
 with epidermolysis bullosa simplex associated with late-onset
 muscular dystrophy." ;
 RL Hum. Mol. Genet. 5:1539-1546(1996),
 RN [4] VARIANT MD-EBS LEU 429 INS.
 DR MEDLINE=21090021; PubMed=11159198;
 DR Bauer J.W., Rouan F., Kofler B., Reznicek G.A., Kornacker I.,
 DR Musz W., Hameister R., Klaeseger A., Huber A., Pohla-Gubo G.,
 RA Wiche G., Utto J., Hinner H.;
 RT "A compound heterozygous one amino-acid insertion/nonsense mutation in
 the plectin gene causes epidermolysis bullosa simplex with plectin
 deficiency." ;
 RL Am. J. Pathol. 158:617-625(2001).
 CC -1- FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTUBULES AND
 CC MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSOMES OR
 CC HEMIDESMOSOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO
 CC MEMBRANE COMPLEXES IN MUSCLE. MAY BE INVOLVED NOT ONLY IN THE
 CC CROSSLINKING AND STABILIZATION OF CYTOKELERATE INTERMEDIATE
 CC FILAMENTS NETWORK, BUT ALSO IN THE REGULATION OF THEIR DYNAMICS.
 CC -1- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2 AND 3: ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN
 CC MUSCLE, HEART, PLACENTA AND SPINAL CORD.
 CC -1- DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN. THE C-TERMINUS WITH
 CC VIMENTIN, DESMIN, GEFAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-
 CC AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
 CC -1- PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM
 CC INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
 CC -1- DISEASE: DEFECTS IN PLEC1 ARE THE CAUSE OF EPIDERMOLYSIS BULLOSA
 CC WITH MUSCULAR DYSTROPHY (MD-EBS OR EB-MD). AN AUTOSOMAL RECESSIVE
 CC DISORDER CHARACTERIZED BY EPIDERMAL BLISTER FORMATION AT THE LEVEL
 CC OF THE HEMIDESMOSOME AND ASSOCIATED LATE-ONSET MUSCULAR DYSTROPHY.
 CC -1- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 CALPONIN-HOMOLOGY (CH) DOMAINS.
 CC -1- SIMILARITY: CONTAINS 33 PLECTIN REPEATS.
 CC -1- SIMILARITY: BELONGS TO THE PLA6IN OR CYTOLINKER FAMILY.
 CC
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 DR EMBL; 254367; CAA9196_1; .
 DR EMBL; US3204; AAB05427_1; .
 DR EMBL; US3310; AAB05428_1; .
 DR EMBL; US3609; AAB05428_1; JOINED.
 DR EMBL; X91053; CAA05765_1; .
 DR HSSP; Q01082; 1BKR.
 DR Genew; HGNC:9069; PLEC1.
 DR MIM: 601282; .
 DR MIM: 226570; .
 DR InterPro; IPR001589; Actinbind_actinin.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR001101; Plectin_repeat.
 DR InterPro; IPR05326; S10_plectin.
 DR InterPro; IPR02017; Spectrin.
 DR Pfam; PF00681; Plectin; 19.
 DR Pfam; PF03501; S10_Plectin; 1.
 DR SMART; SM00033; CH_2.
 DR SMART; SM02503; PLEC; 33.
 DR SMART; SM00150; SPEC; 5.
 DR PROSITE; PS00019; ACTININ_1; FALSE_NEG.
 DR PROSITE; PS00020; ACTININ_2; FALSE_NEG.
 DR PROSITE; PS50021; CH; 2.

GN		LMB2.	
OS	Mus musculus (Mouse).	Best Local Similarity:	41.44%
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Query Match:	21.58%
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DB:	4.21%
OX	NCBI_TaxID=10090;		1
RN	[1]		
SEQUENCE FROM N_A.			
RX	MEDLINE=91139548; PubMed=2102440;	QY	194 ARTGACAGAAATCGAGCCATTCCTTAGTGAAGCATGATGAGAGAGCAGTG 253
RA	Hoeger T.H., Zatiloukal K., Walzenegger I., Krohne G.;	QY	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
RA	"Characterization of a second highly conserved B-type lamin present	Db	162 LeualalysalagluaspglyhisalaValalalylysglieglulysglurhleu 181
RT	in genes previously thought to contain only a single B-type lamin.";	QY	TCTTGGTAACAGAAGCACCTCTACCTCTCTCTCAGACACTATGGTTGATGAA 313
RL	Chromosoma 99:379-390(1990).	QY	[2]
RN		RP	ERRATUM.
RX	MEDLINE=91139548; PubMed=2102440;	QY	182 MetArgValAsp-----LeugluasnArgCysGlnSerLeugluInGlu 195
RA	Hoeger T.H., Zatiloukal K., Walzenegger I., Krohne G.;	QY	314 GCTATACATGAAATACTAACGCTTAT----ACCTAACCTCTTACGACAA 367
RA	Chromosoma 100:67-69(1990).	Db	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CC	- FUNCTION: LAMINS ARE COMPONENTS OF THE NUCLEAR LAMINA, A FIBROUS	QY	196 GluLeuAla---PheserLysserValPheGluGluValarggluthArgrgarg 214
CC	LAYER ON THE NUCLEOPLASMIC SIDE OF THE INNER NUCLEAR MEMBRANE,	QY	254 TCTTGGTAACAGAAGCACCTCTACCTCTCTCAGACACTATGGTTGATGAA 313
CC	WHICH IS THOUGHT TO PROVIDE A FRAMEWORK FOR THE NUCLEAR ENVELOPE	Db	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CC	AND MAY ALSO INTERACT WITH CHROMATIN.	QY	182 MetArgValAsp-----LeugluasnArgCysGlnSerLeugluInGlu 195
CC	- SUBCELLULAR LOCATION: NUCLEOPLASMIC SIDE OF THE INNER NUCLEAR	Db	368 TATAAAGTGTACTGGAAATGATGATGAGGAAGAGATGAGTGGCAGGTGAGC 427
CC	MEMBRANE.	QY	215 HisGluGluArgGluLeuValgluvalaspSerSerArgGlnGlnGlytryAspPheLysMet 234
CC	- ALTERNATIVE PRODUCTS: 2 isoforms: B2 (shown here) and B3 (AC	Db	428 ATAGGAGCCGAGCAGGAGTACTCAAACACCAGAGTACTTAAAG 475
CC	- PAB680); may be produced by alternative splicing.	QY	235 AlaGlnAlaLeuGluAspLeuArgSerGlnHisAspGluGlnValArgLeuTrygVal 254
CC	FARNESYLATION AND PHOSPHORYLATION. INCREASED PHOSPHORYLATION OF	Db	476 ---CTGGAACCACTTGGAGACTCCTGAGTCAGTGGCTTCAGAGATGCGAGAGAACTG 532
CC	THE LAMINS OCCURS BEFORE ENVELOPE DISINTEGRATION AND PROBABLY	QY	255 GluLeuGluGlnThrTyryGlnAlaLysLeuAspAsnAlaLysLeuUserAspGln-- 273
CC	PLAYS A ROLE IN REGULATING LAMIN ASSOCIATIONS.	Db	533 TATCAAATGCGGAGTGGCCCTATACCGCAGGATCACATCCTGAA 592
CC	- MISCELLANEOUS: THE STRUCTURAL INTEGRITY OF THE LAMINA IS STRICTLY	QY	274 -----AspAspLysAlaLahisAlaLaaArgGluGluLeuLysGluAlaArg 289
CC	CONTROLLED BY THE CELL CYCLE, AS SEEN BY THE DISINTEGRATION AND	Db	593 CTGCAGGTGGAAAGACTG-----CACCACTCTCCGGAAAGCAGAACCAAGCTGCA 646
CC	FORMATION OF THE NUCLEAR ENVELOPE IN PROPHASE AND TELOPHASE,	QY	290 MetArgValGluSerLeuSerTyrglnLeuLeuGlyLeuGlyLeuLysGluAla 309
CC	RESPECTIVELY.	Db	647 GAAGCACAGTAGAGAGCTCCGTCAG----- 673
CC	- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.	QY	310 GluAsnHistLeuLysGluLeuLysGluAlaLeuArgGlyGluArgAspLysPheArgLys 329
CC	THIS IS A B TYPE LAMIN.	Db	674 -----AMACACAGGAGAGGGAGGGAGGAGGAGGGCTGAGRCGAGCAGGAG--- 718
CC		QY	330 MetLeuAspAlaLysGluGlnGluMetThrGluValArgAspArgMetGlnGlnLeu 349
DR	EMBL: X54088; CA3A8032.1; -.	Db	719 ----- 724
DR	DR InterPro; IPR01230; Prenyl-site.	QY	350 AlaGluTyrglnGluLeuLeuAspIleLysLeuAspMetGluLeuSerAlaTy 369
DR	DR InterPro; IPR01322; If_tail.	QY	725 CTGGCTGAGGATGGGG---CTCTGACACTGCCTGCTCCAC----- 769
Pfam	Pfam; PF00338; If_tail; 1.	Db	370 ArgLysLeuLeuGluGlyLysGluLysGluLeuSerProSerSerArg 389
DR	DR InterPro; IPR01664; IF.	QY	770 ---TCTGGGGAGGAGGGCAATGCCACCCAGGCTGCTGCTGCTGCTGCTG 826
Pfam	Pfam; PF00332; If_tail; 1.	Db	390 IleThrIleSerArgAlaThrSerSerSerSerSerSerSerSerSerSer 408
DR	DR InterPro; IPR01226; IF; 1.	QY	827 GCACCGAGAAGGGGC-----AGGTCTGCCCAGGCCAATCAGGGAGACGCGCTTG 880
KW	Intermediate filament; Coiled coil; Nuclear protein; Lipoprotein; KW	Db	409 ---GlyGlnArgGlyGlyLysArgArgLeuGluAspThrSerGly---SerProSer 426
KW	Protein phosphorylation; Alternative splicing.	QY	881 TGAGCTGTGAGTCGCCCTCTGGTCAGGCTGCG 916
DR	DR InterPro; IPR01322; If_tail.	Db	427 ArgAlaSerArgValSerSerGlySerArgLeuAla 438
Pfam	Pfam; PF00338; If_tail; 1.	QY	
PROSITE	PROSITE; PS00226; IF; 1.	Db	
MGI	MGI; 96796; Lmnb2.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
InterPro	InterPro; IPR01322; If_tail.	QY	
InterPro	InterPro; IPR01230; Prenyl-site.	Db	
PIR	PIR; S21609; S21609.	QY	
DR	DR Pfam; PF00338; If_tail; 1.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
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Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	QY	
DR	DR InterPro; IPR01230; Prenyl-site.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01664; IF.	Db	
Pfam	Pfam; PF00332; If_tail; 1.	QY	
DR	DR InterPro; IPR01322; If_tail.	Db	
Pfam	Pfam; PF00338; If_tail; 1.	Q	

RL Submitted (MAY-1999) to the EMBL/GenBank/DDJB databases.
 RN [3] SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=Brain stem;
 RX MEDLINE=94075409; PubMed=8253944;
 RA Chan W., Kordell E., Bennett V.;
 RT "440-kD ankyrinB: structure of the major developmentally regulated
 domain and selective localization in unmyelinated axons.";
 RL J. Cell Biol. 123:1463-1473 (1993).
 RN [4] REPEAT
 RF SEQUENCE OF 463-495 FROM N.A.
 RX MEDLINE=92009921; PubMed=183308;
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
 Lux S.E., Ward D., Forget B.G.;
 RT "Isolation and chromosomal localization of a novel nonerythroid
 ankyrin gene.";
 RL Genomics 10:858-866(1991).
 CC -!- FUNCTION: Attach integral membrane proteins to cytoskeletal
 elements. Also bind to cytoskeletal proteins.
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
 PRODUCED BY ALTERNATIVE SPlicing.
 CC -!- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
 CELLS THROUGHOUT THE BRAIN
 CC -!- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
 AND EACH PROSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
 CC -!- SIMILARITY: CONTAINS 23 ANK REPEATS.
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: X56957; CAA40278.1; -
 DR EMBL: X56958; CAA40279.2; -
 DR EMBL: Z226634; CAB42044.1; -
 DR EMBL: M37123; AAA62028.1; -
 PIR: S14533; S14533.
 PIR: A39643; A39643.
 PIR: B39643; B39643.
 PIR: S14569; S14569.
 HSSP: P42771; IDC2.
 Genew: HGNC:493; ANK2.
 DR MM: 106410; -
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00023; ank; 24.
 DR Pfam; PF00531; death; 1.
 DR Prints; PRO1415; ANKIRIN.
 DR SMART; SM00248; ANK; 21.
 DR SMART; SM00005; DEATH; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 20.
 DR PROSITE; PS50297; ANK REP REGION; 1.
 DR PROSITE; PS50017; DEATH DOMAIN; 1.
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
 KW Phosphorylation.
 FT REPEAT 63 92 ANK 1.
 FT REPEAT 96 125 ANK 2.
 FT REPEAT 129 158 ANK 3.
 FT REPEAT 162 191 ANK 4.
 FT REPEAT 193 220 ANK 5.
 FT REPEAT 232 261 ANK 6.
 FT REPEAT 265 294 ANK 7.
 FT REPEAT 298 327 ANK 8.
 FT REPEAT 331 360 ANK 9.
 FT REPEAT 364 393 ANK 10.
 FT REPEAT 397 426 ANK 11.
 FT REPEAT 430 459 ANK 12.
 FT REPEAT 463 492 ANK 13.
 FT REPEAT 495 525 ANK 14.
 FT REPEAT 529 558 ANK 15.
 FT REPEAT 562 591 ANK 16.
 FT REPEAT 595 624 ANK 17.
 FT REPEAT 628 657 ANK 18.
 FT REPEAT 661 690 ANK 19.
 FT REPEAT 694 723 ANK 20.
 FT REPEAT 727 756 ANK 21.
 FT REPEAT 760 789 ANK 22.
 FT REPEAT 793 822 ANK 23.
 FT DOMAIN 1773 1950 REPAT-RICH REGION.
 FT REPEAT 1773 1784 REPEAT A.
 FT REPEAT 1785 1796 REPEAT A.
 FT REPEAT 1797 1808 REPEAT A.
 FT REPEAT 1809 1820 REPEAT A.
 FT REPEAT 1821 1832 REPEAT A.
 FT REPEAT 1833 1844 REPEAT A.
 FT REPEAT 1845 1856 REPEAT A.
 FT REPEAT 1857 1867 REPEAT A (APPROXIMATE).
 FT REPEAT 1868 1879 REPEAT A.
 FT REPEAT 1879 1891 REPEAT A.
 FT REPEAT 1892 1902 REPEAT A (APPROXIMATE).
 FT REPEAT 1903 1914 REPEAT A.
 FT REPEAT 1915 1926 REPEAT A.
 FT REPEAT 1927 1938 REPEAT A.
 FT REPEAT 1939 1950 REPEAT A.
 FT DOMAIN 3536 3620 DEATH.
 FT VARSPIC 1039 1039 Q->QFLGKHLPPAPPPLNEGEISVSRILQLGPPTK
 FT VARSPIC 1444 3528 (IN ISOFORM 2).
 FT CONFLICT 475 476 MISSING (IN ISOFORM 2 AND ISOFORM 3).
 FT CONFLICT 971 971 GQ->S (IN REF. 4).
 FT CONFLICT 3581 3582 I->S (IN REF. 1).
 FT CONFLICT 3586 3586 QY->HA (IN REF. 1).
 FT CONFLICT 3586 3586 T->Y (IN REF. 1).
 SQ SEQUENCE 3924 AA; 430337 MW; 52AC96C42B829D2 CRC64;
 DB US-09-939-293-1 (1-1358) x ANK2_HUMAN (1-3924)
 Alignment Scores:
 Pred. No.: 6.14 Length: 3924
 Score: 102.50 Matches: 87
 Percent Similarity: 35.77% Conservative: 55
 Best Local Similarity: 21.91% Mismatches: 130
 Query Match: 4.19% Indels: 125
 DB: 1 Gaps: 22
 Qy 17 ACAATGGCCCTCGAAGAGTTGGCTG-----TCGGCACCGTAACT 58
 Db 1260 ThrasnvalSerAlaArgPheTrpLeuIleAspCysArgGlnIleGlnGluSerValThr 1279
 Qy 59 TCATCTTCAAG---TACAGACAGTGTTGTTGTCCTGTGCGCAGACTT----- 109
 Db 1280 PheAlaSerGlnValtyrArgGlutIleCysValProTyrmatalysPheVal 1299
 Qy 110 -----AAGAACGGCTG----- 121
 Db 1300 PheAlaLysserHisAspProIleGluIaArgLeuIaGlyCysPheCysMetThrAspasp 1319
 Qy 122 -----TTCTCGAATGATAGACCCATGGAC 148
 Db 1320 LysValAspLysPheIleGluGlnGluAsnPheAlaGluValIleArgSerArgasp 1339
 Qy 149 AAACTGTGACGATGGC-----TTGGAGTAGACCCATGGAC 187
 Db 1340 ValGluValIleGluGlyLysProIleIleAspCysPheGly-----AsnLeu 1356
 Qy 188 GTTCTCATGACAGAAATCAGAGCCTCTCCCTTGTAGTGTAGCATGATGAGGAGA 247
 Db 1357 ValProLeuIleIleSerGlyGlnHisIlePheSerPhePheAlaPhylsGluAsn 1376

QY 248 GCACTGTCITG-----GTRACAGATGGACCCTC-----ACC 280
 :::: ||| |||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1377 ArgLeuProLeuIleValAspSerThrGlnGluProCysGlyArgLeuSer 1396
 QY 281 TTTCTCTCTCGA-----ACCACATATCGCTGATT---GAAGCTTAT-----ACTGAA 325
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1397 PheMetLysGluProLySsErThrArgGlyLeuValHisGlnAlaIleCysAsnLeuAsn 1416
 QY 326 TATACTAAGGCTGTATACCTTAACCTCTTACCCACATAACAGTTACTTGGG 385
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1417 IleThrLeuProIleTyThrLysGluSerGluUserAspGlnIncluGlnGluLile 1436
 QY 386 AAATGANTCAGAGGAGGAAGATGAA-----412
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1437 AspMetThrSerGluLysAsnAspGluLileThrGluUserThrGluThrSerValLeuSer 1456
 QY 413 -----GNGTGCAAGGATGATCATAGGAGCAGAGCTGAGATGACTTCAAAACCCAGAG 466
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1457 HisLeuValAsnGluValProValLeuAlaSerProAspLeuLeuUserGluValSerGlu 1476
 QY 467 TACCTGAAAGCTGAAACCACTTGATGATGCTGCAGTGTGCTCTTCAGAGATGCCA----- 520
 :::: ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1477 --MetLysGlnAsnAspLeuIleThrLysMetThrAlaIleLeuThrThrAspValSerAspLys 1495
 QY 521 -----GCAGAACGCTGCAATGAACTGGCCAGATGAG 553
 :::: ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1496 AlaGlySerIleLysValGluLeuValAsnAlaIleGluLileGluProGlyGluPro 1515
 QY 554 GCCCTCTATACCGCCAGGAATCACATTCAGCTGCTGAACTGCAAGGTTGGAAAGGGTGCAC 613
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1516 PheDluIleLeuIleValGluArg-----ValLysGluAspLeuIleGluLileValAsn 1530
 QY 614 CAGCTCTGCCGGAAGCAGAAACCAAGCTGGCAGAACACAGATAAGAGGAGGCCGCGCAG 673
 :::: ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1531 GluIleLeuArgSerGlyThrCysThrArgAspGluUserSerValGinSerSerArgSer 1550
 QY 674 AAA-----ACACAGGAGGA-----GGGGAGGAGGGCTGAGTCG 709
 :::: ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1551 GluArgGlyLeuValGluLileGluIleValLeuIleAspGluLileGluLileValAla 1570
 QY 710 GAGCAGGAGGCCCTACCTGGTGGAGGTGAGGGCT---GAGCACACTGCCCTGTCRCC 766
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1571 ArgGlnLysAlaProLeuGluIleThrGluThrProCysValGluValArgIleAspLys 1590
 QY 767 CACTCAGTGGGAAAGCAGGGCAGATGCCACCTGCCCAGGGTTGSC-----814
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1591 GluIleLysGlyLysValGluLysAspSerThr-----GlyLeuValAsnTyr 1606
 QY 815 -----ATGACTGTCITGCGACCG-----832
 :::: ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1607 LeuThrAspAspIleAsnThrCysValProLeuProLySsValGluLileLeuThrValCln 1626
 QY 833 AGAGAGGGCCAGGTCTGCCCT-----GCCATCAGGGAG 871
 :::: ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1627 AspLysAlaGlyLysLysCysGluAlaLeuAlaValGlyArgSerSerGlu 1643

Search completed: February 20, 2003, 14:58:18
 Job time : 47.5 secs

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Db 496 Leuthr-ThrSerLeuAlaLagIuLysGlugInglntrAlaGlnIleGlnAsnLeuInthr 515
 Qy 353 TCTCTTACCGACATATACTAACAGTTACTGGAAATGATTCAGAGGGAGATGAA 412
 Db 516 GlntIlyrglMet----- 520
 Qy 413 GTGTCAGGTGATCATAGGAGCCAGAGCTGAGATGACTTCAAACACCAAGAGACTTG 472
 Db 530 LeuVallysValGlnIeUGInGlnAlaAlaGlnSerSerSerSerSerSerSer 549
 Qy 473 AACGCGAAACCACTTGGAAGCCTCA 526
 Db 550 ArgAlaGluIleGluGlnIeUGluAlaLysLeuIysAlavAlaGluGluAlaLysAlaGlu 569
 Qy 527 GCTGCATATCACACTGGCAGATCAGGCCCTATAACCCCCAGGAATCAC----- 577
 Db 570 AlaLusAsnSerLeuLeuIleGluIysGluHsIleGluAlaGluIleGlu 589
 Qy 578 -----ATTCAGCTGGAAACTGAGCTGAGAGGGGCCAGCCTC 619
 Db 590 ValGluIlysGluGluIysLeuGluMetVallysValGlnIeUGInAlaAlaGlnSer 609
 Qy 620 TCCCGAAAGCAGAACCAAGCTGCAAGAAGCAGATCAAAGAACGCTCAGAACAA 679
 Db 610 SerSerSerValGluGlnAlaLeu---ArgAlaGluIleGluIysLeuGluAlaLysLeu 628
 Qy 680 CAGGAGGAAGGGAGGAGCC-----GCTGAGTCGAGCAG 715
 Db 629 GingIuIegIuIgIuIysLysAsnAlaLeuAsnAlaLeuAsnAlaLeuAlaGluIysGluGln 648
 Qy 716 GAG---GCCPACCTGGGTGAG 733
 Db 649 GlntIalAgInIleGlu 655

RESULT 7

ID 069088 PRELIMINARY; PRT; 3164 AA.

AC DT 01-NOV-1995 (T_EMBLrel. 01, Created)
 DT 01-NOV-1996 (T_EMBLrel. 01, last sequence update)
 DT 01-JUN-2002 (T_EMBLrel. 21, Last annotation update)

DE Virion protein.

OS Human herpesvirus 1.

OC dsDNA viruses, no RNA stage; Herpesviridae;

NCBITaxid=10298;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=17;
 RX MEDLINE=8824327; PubMed=2830594;
 RA McGeech D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
 RA McNab D., Perry L.J., Scott J.E., Taylor P.;
 RT "The complete DNA sequence of the long unique region in the genome of
 herpes simplex virus type 1";
 RL Gen. Virol. 69:1531-1574 (1988).
 DR EMBL; D10879; BAA01682.1; -; UI36.
 DR Interpro; IPR005210; Herpes_UR36.
 DR Pfam; PF03586; Herpes_UL36; 1.
 SQ SEQUENCE: 3164 AA; 335017 MW; 2E333F9525F8C71 CRC64;

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
0.806	112.50	3164	86	21	128	85	17

DB: Query Match: 4.66% 12

US-09-939-293-1 (1-1358) x 069088 (1-3164)

Qy 1252 CAGCTGCTCACAGGACAGCTGGGGCAGATCA 1217
 :::::::::::::::::::::GAG 1217

Db 2581 GluleuAlaserAspaspSerGlyGlyProalaProLeuLeuAlaProaspProLeuSer 2600
 Qy 1216 AACACATCACAATACATACAAAGAACATCTACAACACTGACAGCTTCCCTCCCTC 1157
 Db 2601 ProthrAlaAspGlnSerValProthrSerGlnCysAlaProArg-ProProGlyProAl 2620
 Qy 1156 CACAAC-----GGCATCCCAACAGGGGAAACAGACTAACTATT 1115
 Db 2620 avalthrAlaArgGluAlaArgProGlyValProAlaUserThrArgProAla----- 2638
 DE Putative retrotransposon protein.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Qy 434 GCGAGGCTGAGATGACTCAAAACCAAGAGAACGACTTGAAACCACTGGATG 493
Db 1222 -----SerHisIleGluLysAlaAsnGluVal 1335
Qy 494 ACTGAGTGTGGCTCTCAGAGATGCCAGCAGAAGCTGCATACACTGGCGAGATCAG 553
Db 1236 ArgServAlaAspValAspGluLeu----- 1243
Qy 554 GCCTCTATAACGCCAGGATCACATTAGCTGGAACTGCAGGTGAGAGGTGCAC 613
Db 1244 -----AlaArgPhelLeuAspLysThrGluProGluAspaspGluAlaGlu 1259
Qy 614 CAGCCTCCCGAACAGAACCCAG 640
Db 1260 LysLeuLysLysLysMetGluValThrArgAspGlnLeuAlaAspAlaLeuTyrglnLys 1279
Qy 641 --CNGCAGAACAGCATAGAAGAGCTGGTCAGAAAACACAGGAGGAGGAGG 697
Db 1280 GlyLeuAlaMetAlaArgIleGluasnLeuLysGlyGluGlyGluGlyGluGlu 1299
Qy 698 CGGGCTGAGRCGAGCAGGGCCFACCHGCGTGAGGAT 736
Db 1300 -----GluSerSerGlnLysAspLysPheGluGluAsn 1310

RESULT 12
Q924W1 PRELIMINARY; PRT; 356 AA.
ID 0924W1
AC 0924M1; 01-DEC-2001 ('REMBLrel. 19, Created)
DT 01-DEC-2001 ('REMBLrel. 19, Last sequence update)
DT 01-DEC-2001 ('REMBLrel. 19, Last annotation update)
DE ALEX protein
GN Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RN [1] SEQUENCE FROM N.A.
RP MEDLINE=95089824; Pubmed=799727;
RA Kehlenbach, R.H.; Matthey, J.; Huttner, W.B.;
RT "Xlas is a new type of G protein.";
RL Nature 372:804-809(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Kleineke, M.; Kehlenbach, R.H.; Huttner, W.B.;
RT Two overlapping reading frames in a single exon encode interacting
RL proteins - a novel way of gene usage.";
DR EMBL; X84047; CAC39212.1; -
SEQUENCE 356 AA; 37970 MW; 9849ABD0E524A3D CRC64;

Alignment Scores:
Pred. No.: 1.46 Length: 356
Score: 107.00 Matches: 46
Percent Similarity: 38.73% Conservative: 9
Best Local Similarity: 32.39% Mismatches: 45
Query Match: 4.43% Indels: 42
DB: 11 Gaps: 8

US-09-939-293-1 (1-1358) x Q924W1 (1-356)

Qy 946 CAGTGGCCAAAGGCTAAGAACCCAGGTCCAGCGCAGCTGAGCACAGGGCACTCAC 887
Db 72 GlnSerProThrProLys-----ArgSerProGln-ProArgGln-ProLeuProl 87
Qy 886 AGCTCACAAAGGCGCTCGCTGAATGGCCAGGGCAGGACCTG----- 844
Db 87 OARGARGARGSerLysLeuProProGlnProProSerProLeuArgSerProLeuProGln 107
Qy 843 -----CGCCTCTCTGGCACAGCAGCTCAT 815

Db 107 yLeuSerLeuLeuProGluProfileGlnProProGlyLeu-SerLeuGluProGlnArgC 127
Qy 814 GCCAACCTGGCAGGGTCATCGCCCTGCTGCTGCCACTG-----AGTG 767
Db 127 ySglnProLeuLeuGly---GlnProProLeuGluGlnProMetGlnValLeuTrpSerG 146
Qy 766 GGGAGACAGGCCAGGGCCCTCAATCCCACCCAGGTGGCTCCGCA 707
Db 146 LyGluProGlyHis---SerArgLeuLeuGlnPro---LeuGlyHisProSerLeuPro 164
Qy 706 CTCAGCCGCTCCCTCCCTGCTGCTGACGGCTCTCTGCTGCTGCTC 647
Db 164 IaGlnGlnLeuProProGluInPro-----LeuL 174
Qy 646 TGCCAGCTGGTTCTGCTTCGGGAGAGCTGGTGACACTCTCCACCTGCACTTC 587
Db 174 euProAlaGlnSerIleu-----ProAlaGlyGlnProLeuProGlnAlaGlyP 191
Qy 586 CA 585
Db 191 ro 191

RESULT 13
Q99M73 PRELIMINARY; PRT; 603 AA.
ID 099M73
AC 099M73; 01-JUN-2001 ('REMBLrel. 17, Created)
DT 01-JUN-2001 ('REMBLrel. 17, Last sequence update)
DT 01-JUN-2002 ('REMBLrel. 21, Last annotation update)
DE Type II 65KD keratin.
GN KRT2-16.
OS Mus musculus (Mouse).
OC Bokaiyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10980;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEN;
RA Poirier, C.; Yoshiaki, A.; Fujikawa, K.; Guenet, J.-L.; Kusakabe, M.;
RT "Fine mapping of Hagué (Hag), a mouse hair mutation with 2
epileilles.", Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY028607; AAC26233.1; -.
DR MGD; MGI:96700; KIA2-15.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR Pfam; PF00038; filament_1.
DR PRINTS; PRO126; TYPE2KERATIN.
DR PROSITE; PS00226; IF; UNKNOWN_1.
DR SEQUENCE 603 AA; 64987 MW; AFC01BD8D0E780E9 CRC64;

Alignment Scores:
Pred. No.: 1.64 Length: 603
Score: 107.00 Matches: 42
Percent Similarity: 47.70% Conservative: 41
Best Local Similarity: 24.14% Mismatches: 59
Query Match: 4.37% Indels: 32
DB: 11 Gaps: 7

US-09-939-293-1 (1-1358) x Q99M73 (1-603)

Qy 251 GTGCTTGTGCTAACAGATGACCACTCTACTTCTCTCAGACACATAT---GCGTGTG 307
Db 276 ValAlaLeuLysAspValAlaAlaPheLeuAshLysserAspLeuGluAlaAsn 295
Qy 308 ATTGAGCCT-----ACTGAATTACTAAGGGCTTAT-----ACC 346
Db 296 ValAspThrLeuIleGlnGluThrGluLeuLysAlaLeuThrIleGlu 315
Qy 347 TTAATCTCTTACCGACAAATAAGTTACTGGGAATGATTAGGAGGAGA 406
Db 316 MetLeuGlnSerHisLeuSerGluThrSerValIleValLysMetAspSerArgAsp 335


```

Db 343 ValAsnLeuAsnIleLysLeuSerAlaIleLysThrLysTyrLeuIleGluLeuSerVal 362
QY 383 GGGAAATGAATCAGAGAGAGATGAGTGCTGGCGGGTCATAGGACCCAGACT 442
Db 363 LeuLysGluAsnSerSerLysLysGlu-----GluLeuThrSerLysThrLysAla 378
QY 443 GAGATGACTTCACAAACACCAAGAGACTTGACTTGAGCTGGAAACCACTTGATGACTGCAGT 502
Db 379 GluLeuThrAlaAlaLysPheGluGlnPhenLysLysAspThrSerLysThrLysAla 398
QY 503 GGTCTTCAGAGATGGCACAGAACGCTGATCATCAACTGGCCAGATCAGGCCCTATA 562
Db 399 AlaGluAlaIleGluLysValGluGluLysLysLysAlaLysAspGlnLysGluGlu 418
QY 563 ACCCCCAGGAATCAC----- 577
Db 419 AspArgArgAsnThrProThrAsnThrTyrLysThrLeuGluLeuGluLeuIleGluUser 438
QY 578 -----ATTCAGCTCGTGAACTCGAGTG----- 601
Db 439 AspValLysValLysLysAlaGluIleGluLeuValLysGluGluAlaAsnGluUserArg 458
QY 602 -----GAGAGGTGCCACCGACGCTCCCGAACGAGAACCCAGCTGGCACAAAGCA--- 652
Db 459 AsnGluGluIleLysGlnAlaLysGluLysValGluSerLysAlaGluAlaThr 478
QY 653 -----CAGATAGAAGAGCTCCGTCAGAAACACAGGAGGAGGGAGGAGCAGGGCT 703
Db 479 ArgLeuGluLysIleLysThrAspArgLysLysAlaGluGluGluAlaLysArgLysAla 498
QY 704 --GAGTCGGAGGAGGGGCC 721
Db 499 GluGluSerGluLysLysAla 505

```

Search completed: February 20, 2003, 15:01:17
 Job time : 107 secs

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Gencore version 5.1.3

SUMMARIES

OM nucleic - protein search, using frame_plus_n2p model
Run on: February 20, 2003, 14:47:03 ; Search time: 73.5 Seconds

(without alignments) 4923.928 Million cell updates/sec
Title: US-09-939-293-1
Perfect score: 2446
Sequence: 1 ggccgtccqcgctgcaaa.....ggacttacacagaaaaaa 1358

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched:

908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0 Maximum Match 0%
Post-processing: Minimum Match 0% Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-NQDELL-frame+ -n2p-model -DEV=xlp
-Q-/Cn2_1/USPTo_spool/us-09-939-293/runat_200203_111509_14822/app_query.fasta_1.1543
-DB=A_Geneseq_101002 -QFMW=fastaa -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LIST=45 -DOCALLIGR=200 -THR SCORE_PCT =THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFILE_PTO =NORMEXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-NO_XIPXY -NO_MACMAP -LARGESEQS=0 -NEGScores=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 XGAPOP=10 -XGAPEXT=5 -IGAPOP=6 -IGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_101002:
1: /SIDS2/gcadata/geneseq/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDS2/gcadata/geneseq/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDS2/gcadata/geneseq/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1987.DAT:*

9: /SIDS2/gcadata/geneseq/geneseq/geneseq-emb1/AA1988.DAT:*

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11: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1990.DAT:*

12: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS2/gcadata/genedata/geneseq/geneseq-emb1/AA2002.DAT:*

RESULT 1

ID AAB26210 standard; Protein: 239 AA.

AC AAB26210;

DT 23-FEB-2001 (first entry)

DE Human caspase activator Smac.

XX Human; caspase activator; Smac; apoptosis; cancer; autoimmune disease;

KW neurodegenerative disease; mitochondria; S. pneumoniae Spn

OS Homo sapiens.

XX US6110691A.

PN PD 29-AUG-2000.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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GenCore version 5.1.3

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 20, 2003, 14:47:03 ; Search time: 73.5 Seconds

(without alignments) 4923.928 Million cell updates/sec

Title: US-09-939-293-1

Perfect score: 2445

Sequence: 1 ggctgtccgcgcgtgacaa.....ggacttaacacagaaaaaa 1358

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-MDEL=frame+n2p.model -DEV=x1P
-Q-/cnn2_1/USPRO_spool/US099393/runat_2002003_111509_14822/app_query.fasta_1.1543
-DB=A_Geneseq_101002 -QFM=fascan -SUFFIX=rax -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=unman0.cda
-LIST=45 -DOCAALIGN=000 -THR_SCORE=-9CT -THR_MIN=0 -ALIGN=15
-MOD=LOCAL -OPTFM=PCT -NORMEXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09939233 @CNN_1.147_@runat_03/2003_111509_14822 -NCPU=6 -ICPU=3
-NO_XLPPY -NO_NMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=5 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGPPEXT=0.5 -DELEXT=7
```

Database :

```
A_Geneseq_101002:*
1: /SIDS2/gcdata/geneseq/geneseq/geneseq -emb1/AA1980.DAT:*
2: /SIDS2/gcdata/geneseq/geneseq/geneseq -emb1/AA1981.DAT:*
3: /SIDS2/gcdata/geneseq/geneseq/geneseq -emb1/AA1982.DAT:*
4: /SIDS2/gcdata/geneseq/geneseq/geneseq -emb1/AA1983.DAT:*
5: /SIDS2/gcdata/geneseq/geneseq/geneseq -emb1/AA1984.DAT:*
6: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1985.DAT:*
7: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1986.DAT:*
8: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1987.DAT:*
9: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1988.DAT:*
10: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1989.DAT:*
11: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1990.DAT:*
12: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1991.DAT:*
13: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1992.DAT:*
14: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1993.DAT:*
15: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1994.DAT:*
16: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1995.DAT:*
17: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1996.DAT:*
18: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1997.DAT:*
19: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1998.DAT:*
20: /SIDS2/gcdata/geneseq/geneseq -emb1/AA1999.DAT:*
21: /SIDS2/gcdata/geneseq/geneseq -emb1/AA2000.DAT:*
22: /SIDS2/gcdata/geneseq/geneseq -emb1/AA2001.DAT:*
23: /SIDS2/gcdata/geneseq/geneseq -emb1/AA2002.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	SUMMARIES
Description				
1	1201	49.1	239	Human caspase acti
2	1201	49.1	239	Inhibitor of apopt
3	1138	46.5	227	Human pancreatic c
4	879	35.9	186	Human protein sequ
5	190	7.8	40	Inhibitor of apopt
6	186	7.6	23	Inhibitor of apopt
7	164	6.7	35	Inhibitor of apopt
8	141	5.8	30	Inhibitor of apopt
9	125.5	5.2	502	Human WASP protein
10	125.5	5.2	502	Amino acid sequenc
11	125.5	5.2	502	Human Wiscott-Aldr
12	119.5	5.0	317	Human polypeptide
13	119.5	4.6	1485	Novel human diagno
14	115	4.6	1485	A mature human N-a
15	112	4.6	1485	Murine WASP prote
16	111.5	4.6	520	Amino acid sequenc
17	111.5	4.6	22	Novel signal trans
18	111	4.5	401	Drosophila melanog
19	110	4.5	22	Human DITH polype
20	108	4.4	23	Herbicidally activ
21	107.5	4.4	1396	RSPC alpha-helix c
22	107	4.4	589	Streptococcis pneu
23	107	4.4	18	S. pneumoniae RSPC
24	107	4.4	929	Human Zneu2 polype
25	107	4.4	1509	Human Protein SEQ
26	106.5	4.4	23	Human retinal pigm
27	106.5	4.4	344	Human retinal pigm
28	106.5	4.4	370	RSPC protein SEQ
29	106	4.4	520	Murine WASP prote
30	106	4.4	591	Drosophila melanoga
31	104.5	4.3	670	Drosophila melanog
32	104	4.3	663	Human protein sequ
33	104	4.3	749	Drosophila melanog
34	103.5	4.2	317	Human gene 11 enco
35	103.5	4.1	1197	Human polypeptide
36	101.5	4.1	1015	Human protein sequ
37	101	4.1	1297	Human protein sequ
38	101	4.1	441	Mouse ischaemic co
39	101	4.1	1072	Human PKN-2 prote
40	100.5	4.1	1719	Hericidically activ
41	100	4.1	23	Novel human diagno
42	100	4.1	1084	Human protein in seq
43	100	4.1	518	Human ORFX ORF183
44	100	4.1	551	C3 binding protein
45	100	4.1	564	S. pneumoniae SpnA
46	100	4.1	581	Homo sapiens.

ALIGNMENTS

RESULT 1

ID AAB26210

ID AAB26210 standard; Protein: 239 AA.

AC AAB26210;

DT 23-FEB-2001 (first entry)

XX Human caspase activator Smac.

XX Human; caspase activator; Smac; apoptosis; cancer; autoimmune disease;

XX neurodegenerative disease; mitochondria.

XX Homo sapiens.

XX US6110691-A.

XX PD 29-AUG-2000.

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PF 06-JAN-2000: 2000US-0479309.
 XX
 PR 06-JAN-2000: 2000US-0479309.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PT Wang X, Du C;
 XX
 DR WPI; 2000-586350/55.
 DR N-PSDB; ABK94860.
 XX
 PT Novel caspase regulatory polypeptides useful for screening binding agents specific for the polypeptides which are useful for diagnosis and also for treating apoptosis associated diseases
 PT
 XX
 PS Claim 1; column 23-24; 16pp; English.

The present sequence is the human Smac protein. Its coding sequence was isolated by purifying the protein and searching a HeLa cell cDNA library for sequences which bound to probes based upon it. Smac is a mitochondrial protein which is released into the cytosol during apoptosis, and acts as a caspase-3 activator. The protein and its coding sequence can be used to modulate the expression and function of caspases and their activators, and also can be used as drug targets and regulators to promote or inhibit apoptosis in the treatment of cancer and autoimmune and neurodegenerative diseases.

SQ Sequence 239 AA;

Alignment Scores:
 Pred. No.: 3.17e-105 Length: 239
 Score: 1201.00 Matches: 239
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 49.10% Indels: 0
 DB: 21 Gaps: 0

US-09-939-293-1 (1-1358) x AAB26210 (1-239)

QY 20 ATGGGGCTGAGAGTGTGCGCGAGCGTAACITCATTCAGGTACAGACAG 79
 |||||||
 1 MetalAlaLeuLysSerTripleSerArgSerValThiSerPheAlaGlyTyrArgLys 20

Db 80 TGTGTGTTGTTCTCTGTTACTTAAAGAGGGGTTTCAGATTGATAAGA 139
 |||||||
 41 ProThrPheLysThrValThrIleGlyPheGlyValThrLeuCysAlaValProIleAla 60

QY 200 CAGAMATCAGAGCCATACGCCATAGTAGTAGGAAGGATGTGAGGAGAGCAGTGCTTGC 259
 |||||||
 61 GlyLysSerGluProHisSerLeuSerSerGluAlaLeuMetArgArgAlaValSerLeu 80

Db 260 GTAACAGATGACCCCTACCTCTCTCAGACACATATGGTTGATGAACTT 319
 |||||||
 81 ValThrAspSerThrSerThrPheLeuSerGlnThrAlaLeuLeuGluAlaLeu 100

QY 320 ACTGAGATACTAAGCTGTATACCTCTACTCTCTTACCGAACATAACAGTTA 379
 |||||||
 101 ThrGlyUtyrThrLysAlaValTyrThrLeuThrSerLeuLeuTyrArgGlnThrSerLeu 120

Db 380 CTGGGAAATGAAATCAGGGAGGAAGWGAAGTGTGGCAGGGTCAAGGCCAGA 439
 |||||||
 121 LeuGlyLysSerGluGluLeuPgluValPgluValIleIleGlyAlaArg 140

QY 440 GCTGAGATGACTCTAACACCAACGAGTACTTGAGCTGGAACACTGAGACTGCA 499
 |||||||
 141 AlaGluMetThrSerGlyLysHisGlnGlyUtyrLeuLeuLeuGluThrPheThrAla 160

QY 500 GTTGTGCTTCAGACATGGCAGCACAGCTGCAACTGCCAGATCAGGCCCT 559
 |||||||

RESULT 2
 ID AAU78447 standard; Protein: 239 AA.
 XX
 AAU78447;
 AC
 XX
 DT 18-JUN-2002 (first entry)
 DE Inhibitor of apoptosis (IAP) protein Smac.
 XX
 KW Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2;
 KW Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy;
 XX
 OS Homo sapiens.
 XX
 PN WO200216418-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001WO-US26492.
 XX
 PR 24-AUG-2000; 2000US-227735P.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Alnemri ES;
 XX
 WPI; 2002-304115/34.
 DR N-PSDB; ABK15451.
 XX
 PT Novel Smac Peptides and polynucleotides encoding the peptides, useful for stimulating apoptosis in neoplastic or tumour cell which overexpresses inhibitor of caspase, and for identifying apoptosis modulating compounds -
 XX
 PS Claim 36; Page 73-74; 78pp; English.

The invention relates to an isolated Smac peptide or polypeptide (I) and an isolated nucleic acid (II) encoding (I). Also described is a method of identifying a compound that inhibits apoptosis, comprising:

- (a) separately contacting several cell populations expressing a cytosolic Smac (a Smac isoform that begins with MKSDYF sequence, replacing the mitochondrial targeting sequence (residues 1-55 of (I)), and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting domain) with a compound to be tested for apoptotic inhibiting activity;
- (b) incubating the cell populations with a direct stimulus of the cell death pathway; and
- (c) measuring the specific apoptotic activity of the cell populations, where inhibition of the specific apoptotic activity is indicative that the compound is an inhibitor of apoptosis. (I) and (II) are useful for inducing apoptosis in a cell. The Smac Polypeptide and Polynucleotide are useful for stimulating apoptosis in a neoplastic or tumour cell which overexpresses an inhibitor of caspase, where the inhibitor inhibit activation or activity of caspase-3, caspase-7 or caspase-9. Preferably, the cell overexpresses at least a portion of IAP. (I) is useful for identifying an inhibitor or enhancer of a caspase-mediated apoptosis which involves contacting a cell transformed or transfected with a vector expressing (I) with a candidate inhibitor or candidate enhancer; and detecting cell viability, where an increase in

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submitted to the EMBL Data Library, October 1995
 N; Reference number: Z19500

A; Accession: T23157

A; Status: preliminary; translated from GB/EMBL/DBBJ

A; Molecule type: DNA

A; Residues: 1..1133 <W12>

A; Cross-references: EMBL:Z66514; PIDN:CAA91344.1; GSPPB:GN00021; CESP:F59A2.6

A; Experimental source: clone K0111

C; Genetics:

A; Gene: CESP:F59A2.6

A; Map position: 13q2; 43c3; 107c3; 413c3; 492c3; 567c3; 635c3; 710c3; 738c3; 795c2; 1008c3; 1

A; Alignment Scores:

Pred. No.: 0.197

Score: 116.50

Percent Similarity: 42.73%

Best Local Similarity: 23.79%

Query Match: 4.76%

DB: 2

Gaps: 9

US-09-939-293-1 (1..1358) x T22976 (1..1133)

Qy 197 GCACAGAAATCAGAGCTCATTCCTTAGTAGTGTAGCATGATTGAGGAGAGCTGTCT 256

Db 436 AlaginlysArgSerSerGluGluLeuGluThrAlaAsnGluMetValArgSerLeuThr 455

Qy 257 TTGGTAACAGATAACCCCTCTACCC----- 280

Db 456 AlalThrLeuGluAsnSerSerGluGluLeuGluThrAlaAsnGluMetValArgSerLeuThr 475

Qy 281 -----TTTCCTCTAGACCACTAACGGCTGTGAGCTATTCR--- 322

Db 476 AspLysGluLeuGluAlaAlaArgGlnGlnLysAlaLeuGluGluLeuGluLeuAla 495

Qy 323 -----GATACTAAAGCTGTATACCTTA--ACT 352

Db 496 LeuThrThrSerLeuAlaGluLysGluGluGlnThrAlaAsnGluLeuGlnThr 515

Qy 353 TCTCTTACCGACAACTATAAAGTTACTTGGAAAATGATTGATTGAGGAGGAGATGAA 412

Db 516 GluLysGluGlnMet-----GluValGluLysGluGluLysValGlu 529

Qy 413 GRCGCCAGGTGATAGGACCAAGCAGACGACTCACAAACACCAAGAGACTG 472

Db 530 LeuValLysValGluGlnAlaAlaAlaGlnSerSerSerSerAlaGluGluLeu 549

Qy 473 AACGCTGGAACCACTTGATGACTGCA-----GTTGGCTCTAGAGATGGCACGAGAA 526

Db 550 ArgAlaGluLysGluGlnLeuGluAlaLysLeuAlaAlaGluGlnAlaGlu 569

Qy 527 GCTGCATATCACACGGAGATGGCTCTATACCCGAGATAC----- 577

Db 570 AlaLeuAsnSerLeuLeuAlaGluLysGluHisLeuGlnAlaGluLeuHisGlu 589

Qy 578 -----ATTCAGGTGGTCAACGTCAGCTGGAGAGGAGGACCCAGCTC 619

Db 590 ValGluLysGluGluLysLeuGluMetValLysValGluLeuGluGlnAlaAlaGlnSer 609

Qy 620 TCCCGGAAGCAGAACCAAGCTGGCAGAACGACAGATAGAAGAGCTCGCTCGAGAACCA 679

Db 610 SerSerSerValGluGluLysAlaLeu-----ArgAlaGluGluLysLeuGluAlaGlu 628

Qy 680 CAGGAGGAAGGGAGAGCGG-----GCTGACTCGGAGCAG 715

Db 629 GluGluGluGluLysLysAsnAlaLeuAsnAlaSerLeuAlaGluLysGluGln 648

Qy 716 GAG--GCCTTACCTTCGTGAG 733

Db 649 GluThrAlaGlnIleGlu 655

dystrophin, muscle - chicken
 N; Alternative names: ducheine muscular dystrophy protein

C; Species: Gallus gallus (chicken)

C; Date: 07-Sep-1990 #sequence_revision 27-Jun-1994 #text_change 16-Jul-1999

C; Accession: S02041; S02013; S71487

R; Lemaire, C.; Heilig, R.; Mandel, J.L.

Nucleic Acids Res. 16, 11815-11816, 1988

A; Title: Nucleotide sequence of chicken dystrophin cDNA.

A; Cross-references: EMBL:Y12100; PIDN:CAA31746.1; PID:963370

A; Accession: S02041

A; Status: translation not shown

A; Residues: 1..3660 <LEM>

A; Molecule type: mRNA

A; Residues: 1..3660 <LEM>

A; Note: 1869-HIS, 1885-AIG, and sequences lacking 1171-Met were also found

R; Lemaire, C.; Heilig, R.; Mandel, J.L.

EMBO J. 7, 4157-4162, 1988

A; Title: The chicken dystrophin cDNA: striking conservation of the C-terminal coding

A; Reference number: S02013; MUID:89210800; PMID:3072195

A; Accession: S02013

A; Status: nucleic acid sequence not shown

A; Molecule type: mRNA

A; Residues: 1..3573, HA', 3576-3660 <LEM2>

R; Heilig, R.; Lemaire, C.; Mandel, J.L.

Nucleic Acids Res. 15, 9129-9142, 1987

A; Title: A 230-kD cosmid walk in the Duchenne muscular dystrophy gene: detection of

A; Reference number: S09071; MUID:88067745; PMID:2825128

A; Accession: S71487

A; Molecule type: DNA

C; Comment: Dystrophin is proposed to play a role in anchoring the cytoskeleton to the

C; Superfamily: Defects in dystrophin are responsible for the Duchenne/Becker muscular

C; Keywords: actin binding; calmodulin binding; cytoskeleton; leucine zipper; membran

F; 1..237 /Domain: alpha-actinin actin-binding domain homology <ACT>

F; 253..327 /Region: hinge

F; 340..449 /domain: spectrin/dystrophin repeat homology <SP01>

F; 450..550 /domain: spectrin/dystrophin repeat homology <SP02>

F; 560..669 /domain: spectrin/dystrophin repeat homology <SP03>

F; 670..719 /Region: hinge

F; 720..830 /domain: spectrin/dystrophin repeat homology <SP04>

F; 838..936 /domain: spectrin/dystrophin repeat homology <SP05>

F; 940..1047 /domain: spectrin/dystrophin repeat homology <SP06>

F; 1049..1156 /domain: spectrin/dystrophin repeat homology <SP07>

F; 1150..1265 /domain: spectrin/dystrophin repeat homology <SP08>

F; 1267..1369 /domain: spectrin/dystrophin repeat homology <SP09>

F; 1374..1479 /domain: spectrin/dystrophin repeat homology <SP10>

F; 1480..1570 /domain: spectrin/dystrophin repeat homology #status atypical <SP11>

F; 1577..1678 /domain: spectrin/dystrophin repeat homology <SP12>

F; 1680..1784 /domain: spectrin/dystrophin repeat homology <SP13>

F; 1787..1877 /domain: spectrin/dystrophin repeat homology <SP14>

F; 1878..1984 /domain: spectrin/dystrophin repeat homology <SP15>

F; 1980..2103 /domain: spectrin/dystrophin repeat homology <SP16>

F; 2105..2211 /domain: spectrin/dystrophin repeat homology <SP17>

F; 2211..2319 /domain: spectrin/dystrophin repeat homology <SP18>

F; 2323..2419 /domain: spectrin/dystrophin repeat homology <SP19>

F; 2420..2467 /Region: hinge

F; 2468..2574 /Domain: spectrin/dystrophin repeat homology <SP20>

F; 2576..2683 /Domain: spectrin/dystrophin repeat homology <SP21>

F; 2685..2797 /Domain: spectrin/dystrophin repeat homology <SP22>

F; 2790..2928 /Domain: spectrin/dystrophin repeat homology <SP23>

F; 2930..3037 /Domain: spectrin/dystrophin repeat homology <SP24>

F; 3038..3075 /Region: hinge

F; 3052..3089 /Region: WW repeat homology <WW1>

F; 3070..3357 /Region: cysteine-rich

F; 3181..3502 /Region: leucine zipper motif

F; 3547..3568 /Region: leucine zipper motif

Alignment Scores:

Pred. No.: 0.524

Length: 3660

Matches: 56

Conservative: 49

Mismatches: 112

RESULT 4

S02041

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Query Match: 4.58% DB: 1 Indels: 42 Gaps: 8

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

A: Cross-references: GB-L31611; NID:969066; PID:AA37646_1; PID:9469057
R; Ishii, T.; Molioshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akaike, J.; Biol. Chem. 268: 28183; 1993
A: Title: Molecular characterization of the family of the N-methyl-D-aspartate receptor
A: Reference number: A45219; NID:93155102; PMID:8428958
A: Accession: D45219
A: Status: preliminary; not compared with conceptual translation
A: Molecular function: nucleic acid

Qy	125	TCAGAATTGATAAGGACCATGCGACAACTGTGACGATTCGCTTGGAGTAACCCTGTCT	184
		:::	
Db	1193	GluGluLeuGlnLys-----	1197

A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIP1:124265)
C; Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology
F451-879/Domain: glutamyl receptor homology <GRH>

Alignment Scores:
 Pred. No.: 0.569
 Score: 111.00
Percent Similarity: 31.37%

Length: 1323
Matches: 56
Conservative: 8

varley natus.
DB: 2 4,006
US-09-939-293-1 (1-1358) x 178557 (1-1323)
models:
Gaps: 9

QY	365 CAA TAT ACG AGT TAC TGG GAA RTG AAT CAG GAG GAG ATG RA GTG CGC AGGTG ::: :::	424
Db	1252 LeucysSerArgLeuAsnGlyLysCysLysThrIeuGlu-----GluValItp-----	1267

QY 765 -----GGAGACAGGCCAGTGTGCTCAGGCCCTCAATCCCTCACCGAGCTAGGCC 718
 Db 1064 GinProleLeuGlyGlyIala-----GlyGlyProSerAlaGly-AlaProThrI 1081

Qy	605	GAGGTGCAACGCCTCTCCGGAAAGCAGAACCAAGCTGGCAGAAGCAGCATAGAAGAG	664
	:: :: ::	:: ::	
Db	1321	AspArgAsnGlnLleArgGluLeuAlaGlnThrLeuThrAspGlyGlyIleLeuAspGlu	1340

QY	665	CIGGAGACAGAGGAGGAGACGGCTGAGTCGGAGCAGAGGCCTAC	724
Db	1341	LeuIleAsnGluLysLeuGluLysPheAsnThrArgTrpGluGluLeuGlnGluAla	1360

Db 1101 oserAspSerGluAspSerGluSerLeuGlyGlyAlaSerLeuGlyGlyLeuGluProTr 1121
 Qy 639 TTGGTTCTG-----CTTTCGGGAGACTGTGTGCACCT----- 606

Db 1361 ValArgArgLysSerLeuGluGlnSerIleGlnSerAlaGlnGluThrAspLys 1379
RESULT 5
170557

OY 605 - - - - - CTCACCTGC 595
Db 1141 rTrrSerValAspLysLeuGlyGlyTrpAsnAlaGlySerTrrAspTyrLeuProPro 1161
||| |||||

C;Species: *Rattus norvegicus* (Norway rat)
C;date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;accession: 178558; 158158
R;Monyer, H.; Burnashev, N.; Fairie, D. T.; Sammann, R.; Sochava, N."

OY 594 AGTTTACCCGCT-----GAATTCGATTCCTGGGGTTATAGGGCCGTGATC 547
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1161 ggIgLyProIaTrPhisCysArgIcysAlaserLeuGluleuLeuproProAl 1181

A;Title: Developmental and regional expression in the rat brain and function
A;Reference number: 158158; MUD:94206533; PMID:7512349
A;Accession: 17857
A;Status: preliminary; translated from GB/EMBL/DDBT

Db 1181 qHis-----LeuSerCysSerHisAspGlyleuAspGlyGlyTr 1194
QY 486 GGGGTTCCA 477

AAC:Accession: 158158 AAC:Cross References: GB:L31612; NID:g469068; PIDN:AAC37647.1; PID:g469069

RESULT 6
C45219

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